

```

1 CATTGGAGAC CATGGATAAG TACGATGTGA TTAAGGCCAT CGGGCAAGGT
51 GCCTTCGGGA AAGCATACTT AGCTAAAGGG AAATCAGATA GCAAGCACTG
101 TGTCATAAAA GAGATCAATT TTGAAAAGAT GCCCATACAA GAAAAAGAAG
151 CTTCAAAGAA AGAAGTGATT CTTCTGGAAA AGATGAAACA TCCCAACATT
201 GTAGCCTTCT TCAATTCATT TCAAGAGAAT GGCAGGCTGT TTATTGTAAT
251 GGAATATTGT GATGGAGGGG ATCTCATGAA AAGGATCAAT AGACAACGGG
301 GTGTGTTATT TAGTGAAGAT CAGATCCTCG GTTGGTTTGT ACAGATTTCT
351 CTAGGACTAA AACATATTCA TGACAGGAAG ATATTACACA GGGACATAAA
401 AGCTCAGAAC ATTTTCTTGA GCAAGAACGG AATGGTGCCA AAGCTTGGGG
451 ACTTTGGTAT AGCAAGAGTC CTGAATAATT CCATGGAAct TGCTCGAACT
501 TGTATTGGAA CACCTTACTA CCTGTCCCCA GAGATCTGTC AGAATAAACC
551 CTACAACAAT AAAACGGATA TTTGGTCTCT TGGCTGTGTC TTATATGAGC
601 TCTGCACACT TAAACATCCT TTTGAGGGTA ACAAATTACA GCAGCTGGTT
651 CTGAAGATTT GTCAAGCACA TTTTGCCCCA ATATCTCCGG GGTTTTCTCG
701 TGAGCTCCAT TCCTTGATAT CTCAGCTCTT TCAAGTATCT CCTCGAGACC
751 GACCATCCAT AAATTCCATT TTGAAAAGGC CCTTTTtagA GAATCTTATT
801 CCCAAATATT TGACTCCTGA GGTcATTcAG GAAGAATTCA GTCACATGCT
851 TATATGCAGA GCAGGAGCGC CAGCTTCTCG ACATGCTGGG AAGGTGGTCC
901 AGAAGTGTAa AATACAAAAA GTGAGATTCC GGGGAAAGTG CCCACCAAGA
951 TCAAGGATAT CTGTGCCAAT TAAAAGGAAT GCTATATTGC ATAGAAATGA
1001 ATGGAGACCA CCAGCTGGAG CCCAGAAGGC CAGATCTATA AAAATGATAG
1051 AAAGACCCAA AATTGCTGCT GTCTGTGGAC ATTATGATTA TTATTATGCT
1101 CAACCTTGATA TGCTGAGGAG GAGAGCCcAC AAACCAAGTT ATCACCCcTAT
1151 TCCTCAAGAA AATACTGGAG TTGAGGATTA CGGTcAGGAA ACGAGGCATG
1201 GTCCATCCCC AAGTCAATGG CCTGCTGAGT ACCTTCAGAG AAAATTTGAA
1251 GCTCAACAAT ATAAGTTGAA AGTGGAGAAG CAATTGGGTC TTCGTCCATC
1301 TTCTGCCGAG CCAAATTACA ACCAGAGACA AGAGCTAAGA AGTAATGGAG
1351 AAGAGCCTAG ATTCCAGGAG CTGCCATTTA GGAAAAACGA AATGAAGGAA
1401 CAGGAATATT GGAAGCAGTT AGAGGAAATA CGCCAACAGT ACCTCAATGA
1451 CATGAAAGAA ATTAGAAAGA AGATGGGGAG AGAACCAGAG GACATTGAAA
1501 AAGACTTGAA ACAATGAGG CTTcAGAAcA CAAAGGAAAG TAAAAATCCA
1551 GAACAGAAAT ATAAAGCTAA GAAGGGGGTA AAATTTGAAA TTAATTTAGA
1601 CAAATGTATT TCTGATGAAA ACATCCTCCA AGAGGAAGAG GCAATGGATA
1651 TACCAAATGA AACTTTGACC TTTGAGGATG GCATGAAGTT TAAGGAATAT
1701 GAATGTGTAA AGGAGCATGG AGATTATACA GACAAAGCAT TTGAAAAACT
1751 TCACTGCCCA GAAGCAGCAT TTACAGAAct GACTTGgCTC AGTTTCCTCT
1801 TCCTGGAATA CTCTCTGCCT CATTTCTTTC TGGAAAAATC TCCATTcAGC
1851 AGGCATCTTA TTGAGGATCT CCTTTGTGCC AACGACTGCT CACTGAAGGA
1901 CTGGAGTGAG AAGGAAATGG AGCTTAGGAC ATAACCCTAC CACTACATAA
1951 ACAAACTTTG GAGAATCAGG AGAGAGTAAA GCCAAAGGAG GAGAGACAGG
2001 TCATGGGGAG GCACAGGAAT TGGCAGCATC AACTGGAAGA GAAAGGCCAG
2051 ATGAGGGTTT TCCACGCAGA CTGTAGTTGC TGTGGGAAAC AGGAGGCAGT
2101 GGGATGGAGG AGCGCCTCAG ACTCTGCTGC AGATGATGGC AGTGGCCGAC
2151 ATCACCTCCA CTGCCCCAC GGGGCCTGAC AGTGAGTCTG TGCTTAGTGT
2201 CAGTCGTcAG GAAGGGAAGA CCAAGGACCC GTACAGCCCA GTGCTCATCC
2251 TGATGTGATA GTCTACTTCT CACTATACAC CCTATAGATC TTGTATCAGA
2301 CACTTTCAAA TATGTTGTTT TGATATCTCA AGAAAAAAA AAAAAAAACA
2351 CTGTCATGCC GTTACGAGCG (SEQ ID NO:1)

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FEATURES:

5'UTR: 1-11
Start Codon: 12
Stop Codon: 1932
3'UTR: 1935

FIGURE 1A

Homologous proteins:
Top 10 BLAST Hits

			Score	E
CRA 18000004898313	/altid=gi 1709251	/def=sp P51954 NEK1_MOUSE ...	389	e-107
CRA 18000005213056	/altid=gi 9297022	/def=sp Q9R0A5 NEK3_MOUSE ...	311	2e-83
CRA 18000005207774	/altid=gi 6754820	/def=ref NP_035978.1 NIMA...	311	3e-83
CRA 18000004929662	/altid=gi 1709253	/def=sp P51956 NEK3_HUMAN ...	285	2e-75
CRA 108000024647614	/altid=gi 12729925	/def=ref XP_003216.2 se...	256	1e-66
CRA 18000005131165	/altid=gi 2570047	/def=emb CAA70436.1 (Y092...	254	3e-66
CRA 18000005199482	/altid=gi 7522642	/def=pir JC7122 serine (t...	254	3e-66
CRA 18000005207775	/altid=gi 6754822	/def=ref NP_035979.1 NIMA...	254	3e-66
CRA 18000004925928	/altid=gi 4507277	/def=ref NP_003148.1 seri...	252	1e-65
CRA 98000043621119	/altid=gi 12852471	/def=dbj BAB29424.1 (AK0...	244	4e-63

BLAST dbEST hits:

gi 12358928	/dataset=dbest /taxon=96...	252	3e-64
gi 4310159	/dataset=dbest /taxon=9606 ...	252	3e-64

EXPRESSION INFORMATION FOR MODULATORY USE:

library source:

From BLAST dbEST hits:

gi|12358928 Lung carcinoma

gi|4310159 Lung carcinoma

library source of cDNA clone:

placenta

FIGURE 1B

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1 MDKYDVIKAI GQGAFGKAYL AKGKSDSKHC VIKEINFEKM PIQEKEASKK
51 EVILLEKMKH PNIVAFFNSF QENGRLFIVM EYCDGGDLMK RINRQRGVLF
101 SEDQILGWV QISL 3LKHIH DRKILHRDIK AQNIFLSKNG MVAKLGDGFI
151 ARVLNNSMEL ARTCTGTPYY LSPEICQNK P YNNKTDIWSL GCVLYELCTL
201 KHPFEGNNLQ QLVLLICQAH FAPISPGFSR ELHSLISQLF QVSPDRPSI
251 NSILKRPFLE NLIPKYLTPE VIQEEFSHML ICRAGAPASR HAGKVVQKCK
301 IQKVRFRGKC PPRSRI SVPI KR NAILHRNE WRPPAGA QKA RSIKMIERPK
351 IAAVCGHYDY YYAQLDMLRR RAHKPSYHPI PQENTGVEDY GQETRHGPSP
401 SQWPAEYLQR KFEAQYK LK VEKQLGLRPS SAEPNYNQRQ ELRSNGEPR
451 FQELPFRKNE MKEQEYWKQL EEIRQQYLND MKEIRKKMGR EPEDIEKDLK
501 QMRLQNTKES KNPEQKYKAK KGVKFEINLD KCISDENILQ EEEAMDIPNE
551 TLTFEDGMKF KEYECVKEHG DYTDKAFEKL HCPEAAFTEL TWLSFLFLEY
601 SLPHFLLKES PFSRHLIEDL LCANDCSLKD WSEKEMELRT (SEQ ID NO:2)

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FEATURES:

[1] PDOC00001 PS00001 ASN_GLYCOSYLATION

N-glycosylation site

Number of matches: 3

```

1 155-158 NNSM
2 183-186 NKTD
3 549-552 NETL

```

[2] PDOC00005 PS00005 PKC_PHOSPHO_SITE

Protein kinase C phosphorylation site

Number of matches: 7

```

1 48-50 SKK
2 199-201 TLK
3 243-245 SPR
4 342-344 SIK
5 573-575 TDK
6 627-629 SLK
7 632-634 SEK

```

[3] PDOC00006 PS00006 CK2_PHOSPHO_SITE

Casein kinase II phosphorylation site

Number of matches: 9

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1 48-51 SKKE
2 69-72 SFQE
3 243-246 SPRD
4 385-388 TGVE
5 430-433 SSAE
6 444-447 SNGE
7 553-556 TFED
8 627-630 SLKD
9 632-635 SEKE

```

[4] PDOC00007 PS00007 TYR_PHOSPHO_SITE

Tyrosine kinase phosphorylation site

Number of matches: 2

```

1 410-417 RKFEAQY
2 511-517 KNPEQKY

```

[5] PDOC00008 PS00008 MYRISTYL

N-myristoylation site

Number of matches: 4

```

1 97-102 GVLFSE
2 285-290 GAPASR
3 336-341 GAQKAR

```

FIGURE 2A

4 426-431 GLRPSS

[6] PDOC00017 PS00017 ATP_GTP_A
ATP/GTP-binding site motif A (P-loop)
18-25 AYLAKGKS

[7] PDOC00100 PS00107 PROTEIN_KINASE_ATP
Protein kinases ATP-binding region signature
10-33 IGQGAFGKAYLAKGKSDSKHCVIK

[8] PDOC00100 PS00108 PROTEIN_KINASE_ST
Serine/Threonine protein kinases active-site signature
124-136 ILHRDIKAQNIFL

Membrane spanning structure and domains:

Helix	Begin	End	Score	Certainty
1	587	607	0.898	Putative

BLAST Alignment to Top Hit:

>CRA|18000004898313 /altid=gi|1709251 /def=sp|P51954|NEK1_MOUSE
SERINE/THREONINE-PROTEIN KINASE NEK1 (NIMA-RELATED
PROTEIN KINASE 1) /org=NIMA-RELATED PROTEIN KINASE 1
/dataset=nraa /length=774
Length = 774

Score = 389 bits (988), Expect = e-107
Identities = 239/631 (37%), Positives = 350/631 (54%), Gaps =
74/631 (11%)
Frame = +1

Query: 1 MDKYDVIKAIQGAFGKAYLAKGKSDSKHCVIKEINFEMPIQEKEASKKEVILKMKH 180
M+KY ++ IG+G+FGKA L K D +H VIKEIN +M +E++ S++EV +L MKH
Sbjct: 1 MEKYVRLQKIGEGSFGKAVLVKSTEDGRHYVIKEINISRMSDKERQESRRREAVLANMKH 60

Query: 181 PNIVAFFNSFQENGRLFIVMEYCDGGDLMKRINRQRGVLFSEDQILGWVQISLGLKHH 360
PNIV + SF+ENG L+IVM+YC+GGDL KRIN Q+G LF EDQIL WFWQI L LKH+H
Sbjct: 61 PNIVQYKESFEENGSLYIVMDYCEGGDLFKRINAQKGALFQEDQILDWFWQICLALKHHVH 120

Query: 361 DRKILHRDIKAQNIFLSKNGMVAKLGDGFIARVLNNSMELARTCIGTPYYLSPEICQNK 540
DRKILHRDIK+QNIFL+K+G V +LGDGFIARVLN+++ELARTCIGTPYYLSPEIC+NKP
Sbjct: 121 DRKILHRDIKSQNIIFLTKDGTV-QLGDGFIARVLNSTVELARTCIGTPYYLSPEICENKP 179

Query: 541 YNNKTDIWSLGCVLVELCTLKHPFEGNNLQQLVLKICQAHFAPISPGFSRELHSLISQLF 720
YNNK+DIW+LGCVLVELCTLKH FE N++ LVLKI F P+SP +S +L SL+SQLF
Sbjct: 180 YNNKSDIWALGCVLVELCTLKHA FEAGNMKNLVLKIISGSFPPVSPHYSYDLRSLLSQLF 239

Query: 721 QVSPDRPSINSILKRPFLNLIPIKYLTPEVIQEEFSHMLICRAG----- 855
+ +PRDRPS+NSIL++ F+ I K+L+P++I EEF + + G
Sbjct: 240 KRNPDRPSVNSILEKGFIKRIEFLSPQLIAEEFCLKTLKFGPQPLPGKRPASGQGV 299

Query: 856 -----APASRHAGKVQKCKIQKVRFRGKCPPRSRI--VPIKRNAILHRNEWRP 999
PA+++ + K K K PP+ + + +P+K+ ++ E R
Sbjct: 300 SSFVPAQKITKPAAKYGVPLTYKKYGDKKLLEKKPPPKHKQAHQIPVKK---MNSGEERK 356

Query: 1000 PAG--AQKARSIMIERPKIAAVCGHYDYAQLDMLRR-----RAHKPSYHPIP 1143
A K R ++ IE+ K + + + ++R RA + + +
Sbjct: 357 KMSEEAARKRRLEFIEKEKKQ---KDQIRFLKAEQMKRQEKQRLERINRAREQGWRNVL 412

Query: 1144 QENTGVE---DYGQETRHGSPSPSQWPAEYLQRKFEAQYKLVKVEQLGLRPSSAEPN 1311
+ E +G PSP +Y + Y ++ LR E +
Sbjct: 413 RAGGSGEVKASFFGIGGAVSPSPSPRGQY-----EHYHAIFDQMQLRAEDNEARWK 465
Query: 1312 -----QRQELRSNGEEP-RFQELPFRKNEMKEQ-----YWKQLEEIRQQYLN 1437

FIGURE 2B

```

      +RQ+      E  + +E  RK E  + +      Y +L +IR Q  N
Sbjct: 466  GGIYGRWLPERQKGHLAVERANQVEEFLQRKREAMQNKARAEGHVVYLARLRQIRLQNFN 525

Query: 1438  DMKEIRKKMGREPEDI-----EKDLKQMLRLQNTKESKNPEQ---KYKAKKGVKFE 1578
      + ++I+ K+  E ++      E D++ +++++ K  N      K + ++ K
Sbjct: 526  ERQQIKAKLRGENKEADGTGKGQEATEETDMRLKKMESLKAQTNARA AVLKEQLERKRKEA 585

Query: 1579  INLDKCISDENILQEEAMDIPNETLTFEDG 1671
      +K + +E+++ ++ D+P      E G
Sbjct: 586  YEREKKVWEEHLVARVKSSDVPLPLELLETG 616 (SEQ ID NO:4)

```

HMM results:

Scores for sequence family classification (score includes all domains):

Model	Description	Score	E-value	N
PF00069	Eukaryotic protein kinase domain	299.8	3.4e-86	1
CE00022	CE00022 MAGUK_subfamily_d	28.3	3e-08	1
CE00031	CE00031 VEGFR	21.6	1.3e-06	1
CE00359	E00359 bone_morphogenetic_protein_receptor	8.8	0.081	1
CE00203	CE00203 ERBB_RECEPTOR	2.2	2.9	1
CE00220	E00220 ACTIVIN_RECEPTOR	2.0	5.7	1
CE00287	CE00287 PTK_Eph_orphan_receptor	-2.0	4.3e-08	1
CE00292	CE00292 PTK_membrane_span	-9.2	1.2e-08	1
CE00291	CE00291 PTK_fgfr_receptor	-50.8	8.8e-06	1
CE00289	CE00289 PTK_PDGFR_receptor	-64.6	0.17	1
CE00290	CE00290 PTK_Trk_family	-80.7	6e-10	1
CE00286	E00286 PTK_EGF_receptor	-84.2	5.8e-06	1
CE00288	CE00288 PTK_Insulin_receptor	-175.5	2.9e-05	1
CE00016	CE00016 GSK_glycogen_synthase_kinase	-218.2	0.00014	1

Parsed for domains:

Model	Domain	seq-f	seq-t	hmm-f	hmm-t	score	E-value
CE00289	1/1	3	103 ..	1	109 []	-64.6	0.17
CE00220	1/1	124	141 ..	340	357 ..	2.0	5.7
CE00203	1/1	106	154 ..	843	890 ..	2.2	2.9
CE00359	1/1	124	175 ..	272	326 ..	8.8	0.081
CE00022	1/1	120	195 ..	138	217 ..	28.3	3e-08
CE00031	1/1	111	200 ..	1054	1144 ..	21.6	1.3e-06
CE00286	1/1	7	236 ..	1	263 []	-84.2	5.8e-06
CE00288	1/1	6	253 ..	1	269 []	-175.5	2.9e-05
CE00287	1/1	4	254 ..	1	260 []	-2.0	4.3e-08
CE00291	1/1	8	257 ..	1	285 []	-50.8	8.8e-06
CE00292	1/1	6	257 ..	1	288 []	-9.2	1.2e-08
CE00290	1/1	7	257 ..	1	282 []	-80.7	6e-10
PF00069	1/1	4	259 ..	1	278 []	299.8	3.4e-86
CE00016	1/1	1	324 [.	1	433 []	-218.2	0.00014

FIGURE 2C

1	CTTGGCAGGC	CGCCGCTGTG	GCCCAAAGAG	TAGGAAGCCG	TTCCAGTCTC
51	ACGTCCACCT	TTTGGCAATA	TTTGAGACCT	TGTACAAGAA	ACACTCTTCC
101	TGTATCAGTT	TAGCTCATTT	GTAAAACTGG	GAGACTACTG	CCTTGACGGG
151	TTGTAAAGAA	AAGAGAGAAC	GTTTGCGAAG	CGTCTGGTGC	ACCTTAAGCA
201	AGAGCGGGGA	GCGCTACTGT	AGACTGCAAA	GCAAAGGAAT	CCCGACCCAA
251	GGCAACGGGA	CGGTTGCGGG	GTGACTCTGC	CGGGTCTCCA	AACTCCCTGG
301	CGCCTGACCC	TGCCTCGAGG	TGGACTGGTC	CCCAGGCCAT	TCCAGACCCG
351	CGCCCCGCC	GCGTTTCCTT	GCGCGGCTCC	GCCCCGGCCG	CAGGGAGGCG
401	CAGCGGCCCC	GGGAACCCGG	ATCCTTCCGG	GACGCTTCGT	TGGCCCCGCG
451	GAGCCGGCGG	AGCAGGTACG	CTTGCAAGGG	CCGCCCTTAG	TTCTTGCCCG
501	GAGCCGCCAC	AGGGCTTCGG	GAGCTCGGCA	GGGTGGGGGA	AAGGGATGGA
551	GTTTCGGCCT	GGGGCGGCGG	GGGCGGCCCA	GAAAAGGCCT	AGCGTCCTGG
601	GCTGTGTGGT	TGTAGCGTCC	AGGGCGCGTC	GGTCTCTATG	GCAACGCTCC
651	ACACGCGGAG	GTCGGGTACG	GGTAAGCGTC	TTGCCACTCA	CCCGCGGCCG
701	CTTCCAGGGG	CGGCCCTAGG	GGAGAAGGAA	TTTTCTAAT	TTGGGGGCTT
751	CCACCCTTTG	GTGCCACTTG	GGCGGGAGGG	TCGCGGGCCC	TCAGTTCCCG
801	GCGAGTCACC	CCCGGCCCCA	AGTCCGTATG	CGTCTCTCTC	AGAACCCGAT
851	CCTCCGGTGT	CTGCAGCCTC	TCCTGGCTGC	GGAGCTGGTT	CCCAGCCCCC
901	TGCAACCCAG	TACCGACTTC	CCACCCTGAC	GTAAAATTAT	TCGAAAACAA
951	GCCCCCTGCT	CACCCCATTA	ACAACAACAA	CAAACTGTAT	TTATGCCCTA
1001	ACTGTAGCAT	AAAGAGGAAA	TAGAAGGAAA	GCAATAAGTA	AGAAAGTACA
1051	TATTTCAATC	TGAAAAATGCT	TGGCACTACT	ACCCTTGGA	AATGTAGAGA
1101	AGTAGCCAGT	AGCCGCGCCT	GGGGAGTCGC	CTGAACGTGA	CGGCAGCAAA
1151	TGCAGATTGT	TGGGTCTCCG	GGACCAGGAG	CAGCGTGGCC	AGTGAAGCGC
1201	GTGGTTTTCC	CAAATGGTGA	ACAATTCTTG	GTAAACCTCC	AAACCGAAGT
1251	GCAATCAAGC	CTTGATTTAC	ATGTAGTTGC	ATTCTCTGAA	AAAAAAAAGA
1301	AGTGTTCAAT	AAAACTGCAA	AAATACTTAG	CATTTTCGATG	TAAAATAGAG
1351	TTTGTTTCTA	GCCACAAACG	GATTTTTCCA	CGCACAGGAA	TGTATAGGAA
1401	GACTCTCCAA	GATTGTAGGG	CCGCGGGGTA	ATCCTTTATT	GTGCGGGACT
1451	GTCTCTCGAA	TCGCAGAATC	CTACCATCTC	AGGCCCAAC	CACCTGTAAA
1501	CCTCATGCCT	CTGAATCTTG	GGGAAACAGC	TTCCCCACCC	CCATATATTT
1551	CCAGAATTCC	CCCTAGGGGG	CAGTACGTCC	CCACTAAGAA	AGGCTGAACT
1601	ATAAAAGTGC	ACAAGCCTAA	GGACATTCCT	GCTTTATAAA	GGTGCGAAAC
1651	ACCGGATATA	GTATCTTTCA	TTCTCAGAAC	AAACTTGCAA	AACAGGTATT
1701	GTTATTCCAT	TTTAGAAATT	AGGAAAGTGA	GGTTTTGCCA	GGTTAAGTGA
1751	CTTACCCGAG	AATACAGGGC	AAAAGTGTAT	CAAAGCTGAG	CTATGACCCG
1801	TGTCTGACCA	AGAAACTCTG	TCTCATTTCA	GTTATCTGTG	GCCACAAAGA
1851	AAGTTATTTG	TCTCTGTCTT	GGCAAGGCTG	GGAGGAAAGT	TTTAGCTAAG
1901	TGAGTTCTTT	TACACTTTAG	TCATCAGTTT	TCTGACTTTG	TTAGTCTTTA
1951	TGAGACGTGT	GTGATAAATT	TACATTACTC	TAATTCCAGG	AAACTCAGCC
2001	CATTGGAGAC	CATGGATAAG	TACGATGTGA	TTAAGGCCAT	CGGGCAAGGT
2051	GCCTTCGGGA	AAGCATACTT	AGCTAAAGGG	AAATCAGATA	GCAAGCACTG
2101	TGTCATAAAA	GAGATCAATT	TTGAAAAGGT	AAAGTTAAGT	TCAAATTTCT
2151	GTTAATTTTC	AGTGGGATAT	TCAGCTGGCT	TTTAATCCAA	TATAAAAAGG
2201	AAATTTTTAT	TTTTTATAAT	TTCGAATTTT	AAGCCATAAT	TGATTTTTGT
2251	TAATTCAACC	TCCTAAGTCC	ATTGTCCAAA	CAGCAACCAA	TGATCTCATT
2301	TTTAAAAAGA	GGCTGGACGC	ACTGGCTCAC	CCCTGTAATC	CCAGCACTTT
2351	GGATGGCCAA	GGTGGGAGGA	TTGTGTGAAG	CCAGGAGTTC	GAGATAGCCT
2401	GGGCAACATA	GCAAGACCCT	GTCCCTGCTA	AAAAAAAATT	TTTTTAATGA
2451	AAATAGAAAA	GAAATAAGAT	CACATCCCTG	TGGCTCCTAT	GGCCCTCCTT
2501	AGGGTGCCCT	GCAAGGCCCT	GTGAGATGCC	AGCCTCCTCT	GTTGCCCTGA
2551	CTTTTCTCTG	TGGTGCACTT	CCTCTCTCCT	TATTCAGGTC	CTCTACGAGG
2601	GGTTTTCTGC	AAACATCCTA	GCTAGAGTAG	ACCCCCAGCC	ACAATCACAC
2651	CTTATCACCT	TATCACACCA	CCTTGTTTCC	TGGTTTCTTT	TTTGTTTTCT
2701	TTTCTTTTCT	TTTTTTAGAC	GGAGTCTCGC	TCTGTCACCT	AGGCTGGAGT
2751	GCAGTGGCAT	GATCTTGGCT	CAGTCAATC	TCCACCTCCG	GGATTCAAGC
2801	AATTCTCCCA	CTTCAGCCTC	CTGAATAGCT	GGGACTACAG	GTGCATGCCA
2851	CCATGCCTGG	ATAATTTTTT	GTATTTTTAG	TAGAGATGGA	GTTTCACCAT

FIGURE 3A

2901	GTTGCCCAGG	CTGGTCTTGA	ACTCCTGAGC	TCAAGTGATC	TGCCCCGCTT
2951	GGCCTCCCAA	AGTGCTGGGA	TTACAGGCTT	GAGCCACTGC	TTCTGGCCTG
3001	GTTTATTTTC	TTACTAGCAT	GTATAATGCT	CTGCAATTAC	TTTGCTCTCT
3051	TAATTATTCA	TTTGTTTTATT	GCTTGTCTTC	CTCAGTATGC	AGAACAGTTC
3101	CTGTCACATA	ATAGGTGCTA	AACACATTTA	TTGAGTGCAC	TGAATGAATA
3151	GAGAAAAACT	ATATGTAATT	GTTGGTCTAA	TGATTTTGGA	AAATAAATAT
3201	AGTTAATTAA	AAATTAATAA	TTTTTGCTAA	ATCCACCTTG	GTCAGTGTTT
3251	ATGTCACCTT	CTTTAGTGAT	ATGTTCAATT	CATAATATAT	TGGGACAACA
3301	ATGTCCATTG	TTTGCTAGAA	TTAATTCTAA	GGCAAGTCTT	GTTGGTCAGC
3351	TTCTAGAGGA	TTTATAAATG	AGAGTAGCAT	AAAAAGTTCC	ATACAAAGTG
3401	TGTGCAAAAT	GGACTACCCA	AGTTACACCA	TATGAATATA	CTTAATGCCA
3451	TTGAACTGTA	CACTTAAAAA	TCGTTAAAAA	GATATAAATT	TTATCTTACC
3501	ACAAAAAATT	GCAAGAAAAA	CTACCCAAAC	TTAAAGCTCA	AGAGTAGATG
3551	ACTGGCTTCC	AGGGATAATG	ATTTATTTCC	CAATATAGGT	CTCTTTTTGT
3601	GAATCCATGG	CATATTCATA	ATAATGTCCT	CTTATTCTAG	TGGCCCCGAA
3651	TAGCTTCCTC	CCATGACATT	ATTCTGCTCA	CTCTCTTTTG	TTTATCTGAC
3701	TGCTCTCCCT	CAGGCTTATC	TCTGTCTTCG	CCCTGTGTAT	GTCTCAACC
3751	ATGTGTCCTT	TTCTGATTTT	CTTTTTCTGT	CCATTGTCAC	CTAAACTGCC
3801	CCACTTCAGT	GTTTACCAAT	AAGTAGATCT	CTCTTAAATC	TCTGTCTCTA
3851	CCCCTGGCAT	CTTTCAGTAC	CCTAGTCTCG	CATTTCTTCT	GCCAGCTAGA
3901	TAACCTTCAGG	TAATATCTGT	GGTTTTGTTT	TGAGGTGGAG	TCTCGCTCTG
3951	TCGCCCAGGC	TGGAGTGCAG	TGGTGCCATC	TCGGCTCACT	GCAAGCTCTG
4001	CCTCCCAGGT	TCATGCCATT	CTCCTGCCTC	AGCCTCCCGA	GTAGCTGGGA
4051	CTACAGGCGC	CCGCCACCAC	GCCTGGCTAA	TTTTTTGTAT	TTTTAGTAGA
4101	GACGGGGTTT	CACTGTGTTA	GCTAGGATGG	TCTCAATCTC	CTGACTTCGT
4151	GATCCACCCG	CCTCGGCCTC	CCAAAGTGCT	GGGATTACAG	GCATGAGCCA
4201	CCACACCCAT	CCAACATCTA	TGTTATTAAT	CTATTGCTGT	GTAGCATATT
4251	ACCCCAAAC	TAGTGGCTTA	AAGAATAAAC	ATTTATTGTC	TCAGAGATCC
4301	TGTGCATCAA	GAATTTAGGA	TGACGATCAT	TGAGACCACC	TTGGAGGCTC
4351	GGTATCACAA	TTGTACCCAA	AAACAAGTAT	TAATAGTGAT	TCTTCCTTGT
4401	TGTAAGCAGA	CCCACTTCAC	CTCCTATGTG	CTGCGCTGTA	TTAATGTCAT
4451	CAGTGTCCTT	ATGGTTGCCA	GCCTGAAAAC	CTTGGGATCG	TTTGTGAGCT
4501	TATTCCTTCT	CCACATTCAA	TTATTTGGCG	AATACTGTTG	ACTCTTCCTC
4551	TTCTTGAAT	TTGCTTCAGT	CCTTTTGTCG	AGGCCCTGGG	TCACTTGGAT
4601	CCTTCAAGTG	GCTCCAGCCC	AATTTTGATA	ATGCTCCAGC	CATGCCCCCA
4651	AACCTTCACT	GGGACAGAGG	CTGTAAAGAA	AGAGTTGCCT	AGGTTTGACT
4701	ACATAAAAA	AGAAAAAGTT	TGTATGTCAA	AACAAACACT	ATAAATAAAT
4751	TCAAAGAAAT	CGAGAAGGTG	CCAAAAATAT	TTGCAAGTAT	TGACTTAATG
4801	GTGTTAGCCT	TTTATTAAAT	CAATAAAAAG	ATAAAATCCA	TATATGAAGT
4851	CATCGTACAA	AAATTTGAAA	CTCAGTAGAA	AACATAAGAA	TTAGGAGTTT
4901	ATTCAAAGAA	AAACCCACAA	GATAAACAGT	TAGAAAACAA	ATGTCCAACA
4951	GTAGGTAATT	TGTTAAGTAA	TTTATAAAAA	ACTAAGTGGC	TATTAGCAAT
5001	CATGTTGTAG	GTGAAGCATT	GACATGGGAA	AATTTCAATG	TTTGCAATGT
5051	TTGAGAAAA	AGTAAGTGTA	AAATAATATA	ATCTTTGGAA	AAATATATAT
5101	ATTCTCCATA	TATATGTATA	CCTACAAATA	TGTTCAATATA	TGTACAAAGA
5151	AAGACACAAA	TTGTTATTAT	TGAGGTAGAA	AGTGCGGTTT	GCCTTGTGCA
5201	TTTTTTTTGA	GACAGGATTT	CATTCTGTTG	CCCAGGCAGG	AGTGCAGTGA
5251	CATCATCATG	GCTCACTGTA	ACCTTGAACA	AGCCATCCTC	CTGCCTCAGC
5301	CTCCTGAGTA	GCTAGGACTG	CAGGCATGCG	CCACCACACC	CAGCTAATTT
5351	TGAAATTGTT	TTTAGAGACA	GGATCTTGCT	ATGTTGCCCA	GGCTGGCCTC
5401	AAGTGATCCT	CCCACCTTGG	CCTCCCAAAG	TGCTGGGATT	ACAGGTGTTA
5451	GCCACTGTGC	CTGGTCTGCC	TTGTGCTTTT	ATATTGTTTC	ACTCTTCAGA
5501	GAAGTTTTGA	GACCCTCTCT	GATTTGCTCC	AAAACACAG	CTCCTATCAC
5551	ATACCCTACT	TTTTTTCCCC	ACTCCAGCCT	CTGCATTTGC	TTCTGGGGCT
5601	ACTTCTTCCA	AGGTCGTTGC	CTGCTGATCT	CCCAGCATCA	AGATCCCACT
5651	TGTTCAAGGC	TGAGCTCTAC	CATACCTCCA	GAATCCTCCC	ACTCTAAAGA
5701	ATTTATCCTT	CTCTGTAAAC	TTGCATAACT	TTTATTGGAA	CCTCTGTTAT
5751	AGTACTGACT	GCTTCTTTTC	TGGACATGCT	TTGGCTGTTT	ATTTTGTGCC

FIGURE 3B

5801	TTCTCCTCCT	TATTTAGCTG	TAATATGTTT	TGTGAGGACC	GAGTCCATGT
5851	GTGTTTTGTG	CTGGTATTCC	ACACAGCACC	TAATGCTTGG	TGCCAGGAGA
5901	TATTTCAATA	CTTCTTATTG	GATAGATGAT	TCACTGGACA	GATGCTTTCA
5951	GGCCCTCTTG	CTCTACTGTG	AAGCTGGTAT	ATACTTAGGA	ATTATAAAAC
6001	CATTTTAATT	CTATGTAAAG	AGAAAATATT	TGAGAGGTGA	ATCTCTATAA
6051	AAATGTACAT	TAACATTACT	GCATTTCTAT	GCATCTCTCC	CATTCTTTAG
6101	TATAATCAAA	AATTGACTAT	ATTTTTCTAA	TAGAGCACCA	ATTTTTTCATC
6151	ACTTTACTCA	TGAACACTC	TTGTCACTAT	GCCATAAATA	AGTAGAATCT
6201	TATATTAGAC	CTCATTATTC	TTGTTTTCCC	ATATCTGTTT	ATGTTATCGA
6251	ATTTACCTAT	AACATCTGTG	TCACAATATT	AACATTTATT	ACTTCTTTCT
6301	TCCTATCTAC	TCTCATGTAG	TTTTTCATTA	CTTCTTATCT	AGAGAAATTT
6351	ATATTTCTTC	TCTCTAATGC	CTCCCTACTC	CCTACACTAG	ACCCCAAGAAC
6401	TAAATTGCTT	GTTTTCTTAC	AGGTACCAAA	AAGCTAATAT	TTCTCTTATC
6451	ATCCTACCAT	TATCAAGCAT	GTTCTTTTCC	TTCTGGGCTC	AAATAAAAGT
6501	GTTTTATCTT	TCCTCAATTG	TGAAAATAAA	AATGTTCTGT	GTAGAAATTT
6551	TGAAAAGAGC	CAAAGGAGAA	AATAAGACCA	TTTAGAGGAA	AATAAAAAATA
6601	GCATATAACC	TCTTTCTTAA	TCACTATGAA	CACTTTGCTG	AATTTCTCTC
6651	TAGACTATTT	TTAATGTATA	AGTATATAAG	TTATTAGAAT	GATTGGTGTC
6701	ATGGTAGATA	TACTCTTTTT	TTTTTTTTGAG	ACGGAGTCTC	GCTCTGTTGC
6751	CCAGGCTGGA	GTGCAGTGGC	GTGATCTCTG	CTCACTGCAA	TCTCTGCCTC
6801	CCAGGTTCAA	ACAATTCTCC	TGCCTCAGCC	TCCTGAGTAG	CTGGGACTAC
6851	AGGCGCATGC	CACCATGCCT	GGCTAATTTT	TGTATTTTTA	GTAGAAACAG
6901	GCTTTCACTA	TGTTGGCAG	GCTGGTCTCG	AACTACTGAC	TTCTGTATCT
6951	GCCTGCCTTG	GCCTCCCAAA	GTGCTGGGAT	TACAGGTGTG	AGCCACTGCG
7001	CCCAGCCCAG	GTATACTCTT	TTGTAACAGT	TTTTTATATT	AGCAATATAT
7051	TGTGAATATT	TCCTCATCTC	ATTCAATATT	TTTATATAAT	AAAATGTTGT
7101	CATTTAATGA	TATTAATGT	GTTCACTA	ATGATAAAGG	GACCACCTGC
7151	AGGGTGTCCA	TTATATGTCA	CACCATCTCG	GGTGTTTTAT	TATGTATATC
7201	AACTCAATTT	AATCTTCACA	ACCACTTAAA	AGGTAGCTCT	CATTACTCTC
7251	ACTGTACAAG	TGAAAGAGCT	GAGGCTAAAG	AGGTTAAGCA	GTTAGCTCCA
7301	GGATGCACAG	TAATCAGCAG	ATCCATCTAA	GTCTTTCTCT	GCTCTTTCCA
7351	TGATACTACA	TTGCCTCCCT	TTATTTTTAA	TGACTGCATA	GCATTAAAGT
7401	GGTAGCAGGT	CAAAAATACC	ATAATTTAGC	TGGGCATGGT	GGCAAGTGCC
7451	TGTAGTCCCA	GCTATTCTGG	AGGATGAGTT	GGGAGGATCC	CTTGACCCCA
7501	GGAGTTAAAA	TCCAGCTTAG	ACAACATAGC	AGAACTCTGT	CTTAAAAAAA
7551	AAAAAAAAGC	TAGCAAAACA	CCCCTGTAAT	TTATTTAACT	CTTTTTCTAT
7601	TTTCAGATA	TTACATTGTT	TGGTTGGTTT	TTTGGCTACG	ATTCAATAAC
7651	ATTTAATATG	TAAAGTATGA	TTCATTTTTA	TTAAACAAAA	CTATGTATAT
7701	ATGCTTGCCT	ATATATGCAT	GAAATAAAAA	GCTCTAACTA	TAAACAACAG
7751	TTATCCCTAG	GGAATATAGT	ATTAGGTTGG	CGCAAAAGTA	ATTGCATTTT
7801	TGCCATTAAG	AGTAAGGTTA	CCACCTATGG	GCTTTCGTCT	GTGGGCTAGA
7851	TGAGAAAGAA	AGAGGGAAGT	TTCACTTTTA	CCTTATTCAC	TTCTATTTGA
7901	CTTAAAAACA	GCCTGCATTA	TTAGAGTAAC	TTAAAAACTA	GCAATAAAAC
7951	ACTGTAACAA	AGTCTTTTGT	ATGAGAACTC	TTCTGTACCC	TTTTATTATC
8001	TTCTTTGGAT	AAATTTCTAG	AAGAATTAGT	CAAAAATAGG	AACATTTCCC
8051	TCATGCCTGT	AATCCCAGCA	CTTTGGGAGG	CTGAGGCAGC	TAGATCACTT
8101	GAGGCCAGGA	GTTTCGAGAGC	AGCCTGGGCA	ACATGGTGAG	ACCCCATCTC
8151	TACTAAAAAT	ACAAAAAATT	AGCCGGGTAT	GATGGTGCTT	GCCTGTGGTC
8201	TCAGCTACTC	AGGAGGCTGA	GGTGGGAGGA	TCACTTGAGC	TCAGTGGGCA
8251	GAGGCTGCAG	TGAACCAAGA	TCATGCCACT	GCACTCCAGC	CTGGGTGATA
8301	GAGCAAGACC	TTGTCTTAAA	AAAAAAAAAA	AAAAGATTTT	TTCAGCAGGA
8351	TACAGACCCC	CCACAAAAAT	GAACATTTTA	AAGATTCATA	TTATATATTG
8401	TAAAACTGCC	TTCCCAGAAA	TATTTTATCA	ATTTGTGTAG	TTTTACCAGA
8451	AATAAATGAG	TGTCCATTTT	GCTGCTTTCT	GGCCAATAGT	AGTTATTGAC
8501	ATTCTTTTCA	TCTTTGCCAG	TTTCATACAT	GGAATACTAT	ATTACATTTT
8551	GTTTTAGCTT	TTATTCCTTT	TTTTTTTTTT	TTGCAATGGA	GTCTTACTCT
8601	GTCACCCAGG	CTGGAGTGCA	GTGGTGTGAT	TTTGGCTTAC	TGCAGCCTCC
8651	ATCTCCAGG	TTCAAGGGAT	TCTCCTGCCT	CAGCCTCCTG	AGTAGCTGAG

FIGURE 3C

8701	ACCACAGGTG	TGTGCCACCA	CGCCTGGCTA	ATTTTTGTG	TTTTTAGTAG
8751	AGACAGGGTT	TTGCTATGTT	GGCCAGGCTG	GTCTTGAAC	CCTGGCCTCA
8801	AGTGATCTGC	CTGCCTTGGC	TTCCCAAAGA	GCTGGGATTA	CAGGCATGAG
8851	CTACCACACC	CAGCCAAATT	TTGCTTTAGT	TTTTATTCCT	TTGATTACTG
8901	CATGAGATTG	AATATTTTTT	CTATCAGCCA	TTTTATTTTC	TCTTTTTTTT
8951	TCGAGTTGAC	TATTCTTGTA	CTTTGCTATT	TTTCTGTTGG	GGTGTGTC
9001	TTTTTAAAAA	TTATTTGCCA	TCAATTTTTA	TATTATAAAT	ATATTTGTCA
9051	TATATGGTAC	AAATATTGTA	TCTTATCCTT	TTGTTTGTCT	TTTAATTTTG
9101	TTTATAATAT	TCTTTTAAAT	AAATAGTAGT	TAGGAATTTT	TTAAGTTGCT
9151	AAATGTATCC	AGCTGGTAGG	AGTAATTTAG	CTGTTTTTGT	TTTGAAACTC
9201	CTATGTACTG	ACTATACAAT	TTAAATTGGG	GCAGGAAACA	CTGAAGCTTA
9251	GAGGGGTTTA	AGGAACTTAC	TGAAGGATCC	TTCAGCTGAG	ATGTAGGGAA
9301	GCTAGAAATTG	AGAATATTAA	TTTTTAAGAA	GTTCTTAAGT	CTAAATGAGA
9351	ATGAGAAATC	TGGCCAATGT	TGAAGACCTC	TAATGGGTGG	AGGCCCCGTG
9401	GACATCAGAA	AAGCGGGGCA	GTCAGGGGCT	GGAAGTCAGG	GTAGAAATGA
9451	CAAGTCAGCA	AAGCATCAAG	AGTGAGGAAG	AAAAAGTAGA	AATGAGGTGT
9501	GGCCACTGGT	ACTGGCACCA	AACCCCTTGG	CAAGTATTGT	CTATAGGTGA
9551	AAGTAGAACA	AGAAAAACA	CCCAAATACT	TCTAAATGA	AGTCATGCAA
9601	GACAATTTTT	ATTTGAAAT	GAAAAATGTA	GTCATCTTAA	TACAAAAATT
9651	TACTGACCTG	ATTTCTGTGG	GATATGACAC	ATTTTCTTTT	TTTAGATTTT
9701	ATTTGTTTCT	TCTCAGCAGT	GATTGCTCCT	GGAATGTTGC	ATTTTATAAA
9751	AGAATTCCTT	CGCTACTGAA	AGATAGATAT	TAAAATATGG	CTCCATATGG
9801	CTAGACTCTG	AACACGGTAC	CACCAGTCCA	ACTTTTAATA	TAGCAAAACT
9851	TCACCAGAAA	TATTTATTTT	CTTGATGATG	GTTGTCAACA	AACCATTGAT
9901	GAGATGTAGG	GCACTCTGCT	AATTCTAGAA	ATGTTGTTTC	CTGCCATTGA
9951	AAGATCGTTT	TCAAAGTGAC	ATTAAGAGCC	AGTGAAATCC	TAGAGAATTT
10001	TAGATGGAAA	TGAGCAGAAA	GCATGTTCTT	GAAACCAAGT	TAGCTTTATA
10051	GACTACTCTG	TCTCTTAATG	TAATTTAGAT	GCCCATACAA	GAAAAAGAAG
10101	CTTCAAAGAA	AGAAGTGATT	CTTCTGGAAA	AGATGAAACA	TCCCAACATT
10151	GTAGCCTTCT	TCAATTCATT	TCAAGGTTTG	ATTTTCTAAT	ATTTCGTTAAG
10201	TATTTTTATA	AAGTATAGGC	ATGTTGACAT	ATGTAAAAAG	ATTTGTTTCT
10251	AAGGACTGTG	TATAAATTAA	TTTTTGTAAG	TGGGTCATTT	CCCCATTTAC
10301	TTAAATTGCA	GCTTGAGACG	TCCTCGTTAT	TTCTCTCTTA	GTAAGTTTTT
10351	GTAGACGGCT	TTCTTATGTT	TTCTTGTTTT	TCTGCCTCTC	CTTAATTCTC
10401	ACTCTCCCAA	AAAATTAATG	ACTGGCTTAT	TAGCTTCTTT	GCTGTAGTAA
10451	CAACCCCCAA	ATTTAAGTGA	CTTACAATAA	GACACATCTA	TTTCTCACTT
10501	ACATTACATG	CTAGCTGTGG	TGGGCTGGGG	TCTTGAGTCT	GGGGCCAGG
10551	CTGAAGGAGC	AGCTCAGATA	AGGAACGAGC	TGTTCTCATA	AGCAAGAGAA
10601	GAGGGGAAAA	CACAGAGCCC	ACCACACTAT	CGCTCTCAAA	GCCCTGCTAG
10651	GATGTGTGTG	TTTGTGTGTG	TGTGCTGGGG	GGTACTCTGT	TTACATGAGA
10701	TCCTGCATAT	CCTCAGGCAA	CAGATGGGAC	TGTGTAATCC	TCTTACAGAG
10751	AGCCAGCAAA	CAGCCACGCA	CCATAGCCTA	GCACACTGCC	ACGGAGAGGG
10801	GGAGAACTTT	AGGGAAGGAA	GTACCTTCCT	CTGTACACCT	GAATACAATT
10851	CTGCTGACAA	CTTTAGGGAA	GGAAGTCCCT	TCCTCCATAC	ATCTGAATAC
10901	AATTCTGCCT	CCACGCATCA	CTGTAGTCCA	AAGGTAAAAA	ATAAATAATA
10951	AATGAAGGAG	CATTGGTCAG	ACAGCATTCA	TCACTGAAC	TGATACTTAT
11001	TGAGTGCTTA	CTCTATGCCA	GGCATTGTTT	TAGGTGTCAG	GAATATAGCA
11051	GTGAACAAAG	CAGATGAAAA	TCCCTGTTTT	CATGAAATTT	ATATTCTAGT
11101	GGGAAGAGAT	AGACAATAAA	CAAATCTACA	GTATGTCAGG	TGTGTCTTAA
11151	GTTGTGACAG	GGCTGTATGT	GCTGACAGTT	TTATGAAGGG	TCATTTCCCA
11201	GCCCAGCCCC	CAGCGCAGGG	CTGTTTTAAG	ACTGATAATT	AGTTCATGGA
11251	GCAGAAGTGT	TAACCTCAAT	ATCTTCAAGC	ATCATCAGTT	GGGTAAAAAGT
11301	CAGTCAATAA	ATAAATACAG	CCACTGTGTC	TTGAGTATGT	AAACTGTGCA
11351	GAGCACTGTG	TTCTTTACTG	ATTAAGACCG	CTACATTCAA	GGTACTTCTG
11401	TGTGTATGGC	CCTTCTTTGG	CTTCTGGGTA	TTTAAAAAGA	GCTCTTGGGA
11451	CTCTTCTGAG	GTCTTCCTGG	GAGCAGAAAC	GTACACATGG	TCTGGAATTG
11501	GGTTGCATGG	AATAAATTTT	AAGGAAAGCC	ACTGAATAAA	GTGCCCTGCA
11551	TTCTGTCCA	TTGGATACTG	ATAATGCTAT	AAGATGATCT	TTCTCTTCTT

FIGURE 3D

11601	TATTTTGT	GAGATTATTG	TGACTCTCTG	GCTAACTCCT	ACTTATCCTC
11651	AGGCCTTTTC	TGAACTCACA	ATTCAAATTA	CAGCTCCCTT	TGGTTCTCTT
11701	CCACAGCAGT	TGTACTTACA	TATGTCTATT	TATATAATTA	TGAATTTGTT
11751	TCATATTTGT	CGCCCTTTAC	ATGGTAAACT	TAATGAATTT	TGGGGCTCCA
11801	TCTGTTTTGC	TCACCACTTG	ATCCTTGGCA	TGTAGCACAC	AATGGCTGCT
11851	CAATACCTAT	TTACTGAATG	AGCAAATGGA	CTGGACCACT	TTTAGAGACT
11901	GGAGTATTTT	CTTATACCAT	GTGAGATTGA	TTTTTGAGGA	CAGTTTACCA
11951	CTGGAAGCTT	TTGCAGAACT	AAGGTCATTT	TTACAGTATA	CATAACCTCT
12001	GCTGTGTTTG	TTGATACTGT	AAGTTTACAT	TTTCTTATGA	CTCTTTTTAA
12051	GTAGAGCACC	CCTGTGTTTA	GGAAAGCTAG	AGCTATTGTG	ATGCCTTTGA
12101	GTTTGCTTGG	CTGATTGCTG	GGACTTGAAC	TACTGAGCTT	ATCTAAAAGC
12151	CTCAGAGGCC	TTGTAGCCTC	TGCTTTTTAG	AGAGTGTAGG	TAAAGGCTTG
12201	TTTTCCCTCA	AATCGCTTAT	CTCTGATCAT	AAGAACCATG	GCTCTAATGT
12251	TTGTCTATAG	AAAATAGAA	GTTTTGGCCG	GGCGCAGTGG	CTCATGCCTG
12301	TAATCCCAGC	ACCCTGGGAG	GCCGAGGCGG	GCAGATCACC	TGAGGTCAGG
12351	AGTTCAAGAC	CAGCCTGGCC	ATGGTGAAAC	CCCGTCTCTA	CTAAAAATAC
12401	AAAAACGTTT	AGCCGGGCAT	GGTGGTGTGC	ACCTGTAATC	CCAGCTACTT
12451	GCGAGGCTGA	GGCAGGAGAA	TCGCTTGAAC	CTGGGAGGCA	GAGGTTGCAG
12501	TGAGCTGAGA	TTGCGCCACT	GCACTCCAGC	CTGGGCAAGA	AGAGTGAAAC
12551	TCTGTCTCAA	AAAAAAAAAA	AGAAAATAGG	ATGTTTTTAT	TGGTTTGAAG
12601	CAACATAAGA	AAAAAATGA	GAATGTAGTG	ATATTTTCCT	AAGACAAAAT
12651	TAATTCATG	TATATTCAT	CAATAAACAT	TCACTAAGTG	TCTGTTATAT
12701	GCCAGGCATG	TTCTAGGTCT	TGGAGATATA	TCAGCAAACA	AAATAGGCAA
12751	AAATTCCCAT	GCTGTTGTAT	TTGTTTTCTA	TTACTACATA	ACAAATGAAC
12801	ACAAATTTAG	TGGCTTAACA	ACAACACCTA	TTTATTATCT	CTTGATTTCT
12851	GTAGGTCAGA	AGCCTGAGGT	TGGCTTAGCT	GGATTCTCTG	CCCGGAGTCT
12901	CAGCTAGTTG	AAATCAAGGT	GTCAGCTGGG	ACTGTTATCT	GTGGCTCATG
12951	GTCCTCTTCT	AAGCTTATTT	AGGTTGTTAT	AGATTTCAAT	TACTTGCAAT
13001	TGGGTAAATT	GGATCATGGC	TCACTGCAGC	CTTGAACCTC	TGGCCTCAAG
13051	TGATCCTCTC	GCCATGGCCT	CCAAAAGTGC	TGTGAGTACT	GTGCCTGGCC
13101	AGAAAGAGCT	CTTTTACATT	TATTTAAACA	CAGAGTTTTA	TTTTATATTA
13151	CTCTAATGCA	CACATAAAAA	AGAAAATATA	AGCAAAACAA	GTTGGTTAAG
13201	GTATTTCTAA	AATTTATTTAG	GCAGTGAAAA	CATTAAGCCT	GCCGGGTCTA
13251	CAGCAAGTGA	TTGGAAGATG	CCAATGTCTG	TAAGAAACAA	TCTTGATTTT
13301	TTTTTTTTTT	TTTTTTGAGA	CAGTCTTACT	CTGTTGCCCA	GGCTGGAGTG
13351	CAGTGGTGTG	ATTACAGCTC	ACTGCAGCCT	TGACCTTCTG	GGCTTAAGGG
13401	ATCCTCCCAC	CTCAGTCTCC	TGAGTACTGG	GACTACAGGC	ATGTACCCCC
13451	ACACCTGGCT	AATTTTTGAA	TATTTTTTCA	TTATAGAGCC	AGGTTTTTCGC
13501	CATGTTGCCC	AGGCTGGTCT	CAAAACACCTA	AGTTCAAGCA	ATCCACCTGC
13551	CTTAGCCTTG	GCCTCCCAAA	GTGCTGGGAT	TACAGGAGAG	AGCTGCTGCG
13601	CCAGGCCCTT	GATTTTTTAA	AAGTGCATTT	TAGAAATGAAT	TATAATAATT
13651	GTTTAATAAA	TGTTGGAATT	TGACAAATAA	AAAGGTTATT	TAGTGCCCTT
13701	CAATTGTTTT	GAAGTGTCAG	TGATCCATGA	GCTTTACAGC	AGATGGAAAA
13751	TTTGAGAGCA	TAAATGATTT	TTCCAGACAC	TTCCAATAAA	TATAAAATTA
13801	ACAGTGGCTA	ATGGGGGAAA	ATCCTTATTT	TACAGTCAGA	TAATGCTAAT
13851	TGACATTAAG	TAGTTTCTTT	TTTTTTTTTT	TTTTTTTTTT	TTTGACGGAG
13901	TCTCACTCTG	TCACCCAGGC	TGGAGTGCAG	TGGCACAATC	TTGGCTCACT
13951	GCACCTCCAC	CTCCCGGGTT	CAAGCAATTC	TCCTGCCCTA	GCCTCCTGAG
14001	TAGCTGGGAT	TACAGGCGCC	CGCCACCATG	CCTGNNNNNN	NNNNNNNNNN
14051	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN	NNNNNTAATA	TCAGGGATTT
14101	AGAAATAGGA	TGAAATGACA	AGCTAAAGTC	TTTGAGTCTT	AGTTCCTCAG
14151	CTGTAAAGTG	GGCATGGTAC	CATTTACACAG	GAATTGATAC	GAGGATTAGA
14201	AGAGATTAGG	GCTGTGAAGT	GCCTGACACA	CAGATAGTTC	TTGAATCAAA
14251	TGAGGGTAAA	TTGTAGCACT	CATCTGTCTC	ATAAGCCTAA	ACTGCACATG
14301	TATCTATATA	TTCATGACAA	AAATCATTCC	AACACCCAGG	GGCTGTCCAA
14351	AATACATCTC	TATCTCTCTG	TATACCTATT	CCCTCTCCAC	CCCCCAAATC
14401	CTATACAAAT	TCCTCTTCTT	CGGCCGGGCA	CGGTGGCTCA	CGCTTGTAAT
14451	CCCAGAACTT	TGGGAGGCCA	AGGCGGGTGG	ATCACGAGGT	CAGGAGATCG

FIGURE 3E

14501	AGACCACAGT	GAAACCCTGT	CTGTACTAAA	AATACAAAAA	ATTAGCCGGG
14551	CATGGTGGCG	GGCGCCTGTA	GTCCCAGCTA	CTCGGAGAGG	CTGAGGCAGG
14601	AGAATGGCGT	GAACCCAGGA	GGCGGAGCTT	GCAGTGAGCC	GAGATTGCGC
14651	CACTGCACTC	CAGCCCAAGT	GACAGAGCGA	GATTCCGTCT	CAAAAAAAAAA
14701	AAAAAAGGTA	TCTCTGTCAT	GATGAATTTT	TAGTCAGTTT	CTTTCAACAA
14751	AAGCCAGTGT	AAGTTTGAGT	GAGTTGGAGG	TTGGTGAAAA	GGAAGTGAGA
14801	TGAAATAATG	TGTCTCCTCT	GTTCATTAT	TCTGATTCTT	CCATGGTTTT
14851	GAAATTGCCA	TCCCTTCATT	GCTGTGGCAG	ACCTTTTACT	GACTGAGCTT
14901	CAATGACAAG	AAACATCAAT	TCTCCTAAAA	GTAACACATT	CCTGAAAAATA
14951	ACCGATCTCT	AGACATTAAG	GCATATGGGG	AAGCATCTTC	TCAGAACCTT
15001	TCCTAGATCT	CCAGTCTTAC	TTGCATGCGC	TTTCTCCTCA	CCCTCCAGCC
15051	TACAGACTTC	TTACACAGCAC	TTCTCACCCA	ATGCTGAGGG	ACTCCCCAAC
15101	TAGACTTCGC	CTCCTTAACA	GTAGAATGGA	TGGCTTCTTT	GCTTTTTATT
15151	CCTACACAGC	ATTCCTTGCT	TTTGCATGTC	CTCAATAGAA	GTTTGTTAAT
15201	AACTGAATGG	ATCGTCTCTT	AAAGAAGAGA	GGAGGAAAAA	TTGAAATATG
15251	TGAAAGAAGA	TGCATGGTTT	GTGAATTAGA	AGCAACCAAG	GGTAGACACT
15301	GCCAGGTTAC	TGATATCCAC	AGTAAAGTTG	GTTAGGGTAC	TTTAAAGAGT
15351	AGATAGACAA	AAGATAGATA	TTTGCCAAGA	GATTTTGCCA	TTTAATGGGT
15401	ACTACAGGGG	AAAAATGTTAT	CAACAATTGC	TTATAAGACT	GATTTTGCGC
15451	CTTATGTTTT	GTGTTCTTTC	AGGGTTTTTT	TGTTTGTTTG	TTTTTAATGA
15501	ATCCACTCAA	CAAAACATTTA	AGCCCCTTTG	ATGTGCTAAC	TACTGTTTAG
15551	GTACAAAAGA	ATGAAGTGTA	GACAAACAAG	TGAGTAGAAA	TCCTTCTTTT
15601	CTAACAAGAT	CCCAGCTGTT	AGTTGGTTGG	CTAATGAAGA	AAGCTGGTTA
15651	GAGCAGAAAA	TCATCTGTTT	TAGTCTATTC	CAGCAGCTAT	AACAAAAATAC
15701	CATAAACTAG	GTGGCTTATA	AACAGCAGAA	ATTTATTTCT	GGCAGTTCTG
15751	GAGGCTGGGA	AGTGCAAGAT	CAAGGTGCAG	GCAGATTTCAG	TGTCTGGTGA
15801	GGGTTCACTT	TCTGGTTTCT	AGATGGTCCG	CCTCATTTGTG	ACTTCACATG
15851	GTGGAAGGGG	AGAGGGTTCT	CTCTTGACA	GCAATCCATT	AATGTGGGCT
15901	CCACCCTCAT	GACCTAGTCA	CCTTCCAAAA	GCCCTATACC	TCCTAATACC
15951	ATCACTGTGG	GGGTAAAAAT	TTCAACATAT	ACATTTGGGG	AAGACAAAGA
16001	CATTTGGATC	CTAGCAATTA	TACAGACATA	TTTTAACATA	AGAAGACATA
16051	ATCATCCTTT	GAGTGGAAT	GGCCAGGAAA	AAAAAAAAGA	AAAAAAATTT
16101	AAGGAAATGA	CAAGCATTTG	TTAAAGGATA	ATTTCTTTTC	TTTAATACGG
16151	AGCAAGTGTT	TGTGGATAAT	CTGTCCACAA	TCCTTTTAGA	AGTTTTCTAG
16201	TTATATTTCA	TTCATTTTCT	TCAACATTTA	GGTCAATGGT	TATTTATTTA
16251	TTTATTTTTA	AACTCACTGA	GTCCTCCAAA	ATATTCAGCA	TAGCTTTTGG
16301	AGGAATAATC	ACATCTTTTCA	TTTTCTATTC	ATATTTTCATC	AGTTTATGTA
16351	ATAAAGACAA	GAATAACTCA	CTACAGTTCA	AGAAAAATTCA	GAATTATAGT
16401	TGGTAGATTA	TGAGTCCACT	GACTATAGTT	CTGAATTTTC	TTTCTTATGT
16451	AAGTTATGTG	TCTTATTTAG	AATTTCTAGT	CTCTTTTCTT	TAATGTGGAG
16501	CAAGGATTTG	TGGATAGTCT	GTACATAATC	CTTTTAGAAG	TTTTCCAGTT
16551	ATATTTTCAT	CATCCCATCA	ACATTTAGGT	CAATAGCTAT	TTTTTTTAAA
16601	AACTACTCAC	TTTTACTGAG	TCCTCCAAAA	TATTCAGCAT	AGCTTTTGGA
16651	AAATAATCAC	CTTTTCATTTT	CTATTCATAT	TTCATCAGTT	TATGTTACAA
16701	AGACAAGAAT	AAATGGCGTA	AACATATTTG	GGAAAAAACA	AAATGATCTT
16751	GGTAAGATTC	AGTTCAATTG	GTAAGAGCAG	AGGTACTTGG	ACATACTAGA
16801	GAGCCTAGTA	GTATTTAGTG	GTAACGTTGA	TGGGGCAATA	GCAATGGAGA
16851	GTGTCCTGTA	ATCTAGTGAG	TGGTTTAGGC	AGAGGTCAGT	TATAAGAGTT
16901	TCTATTGTAT	TCAACAACAT	AGATAAATAA	GTGCCATATA	AATATGGCTT
16951	TATGCCCAAA	TTCAAGAAGG	GGCTATTAAT	TCTTCCTGGG	GTGTTATGAA
17001	AGAGTCACAG	CTGCTATTTT	TACAGCAGAT	TTCTAACCTC	TCAAAGGAAT
17051	GTATTAATAA	AAATAGCCAA	CATTTCTTAA	ACTCTCATT	TGTACAGGCA
17101	TTATTCTAAG	CATCTGACAT	GGATTAAGTC	ATTTAATCTT	TCCAACAATC
17151	CAAAGAAGAA	ATTTCTATAA	TATTTCCATT	TTACAGATGA	GGTAATGAGG
17201	CACGGAGAAG	TTAAAGTGAC	TTGCCAGAG	TCACAGAGCT	AAGAAATATA
17251	AATGGTATAG	TGGAATTAGA	ACCCAGTCCA	TCTTGATTCC	ACAGCCAGAA
17301	CATGGCTGAT	AAATATCTGA	AATCCTTCCA	GCACCAAATG	ATTCCTTTTC
17351	TTACAGAGAA	TGGCAGGCTG	TTTATTGTAA	TGGAATATTG	TGATGGAGGG

FIGURE 3F

17401	GATCTCATGA	AAAGGATCAA	TAGACAACGG	GGTGTGTTAT	TTAGTGAAGA
17451	TCAGGTA AAA	ACTTCTAATT	TGCTTTTTAA	TTTTATGTAT	GTGTGGTGGG
17501	GGGAGAAATTA	AATTTATAAT	GTCATAAGTA	GTAGACTATG	TTGATATAAA
17551	GCATGTGTTT	TGGTAGACAG	ATTGAAACCA	TAAAATAGTG	GATCAATATT
17601	CTTGGTAGAT	TCAGTCCAGA	ACAAGTTTGC	AATTGAACTT	AAACTGAATT
17651	GTTTTTTAGA	GAGTGAGATT	TTCTTGAGAA	AAGATAATCT	GTTTGGAAAA
17701	TCTCATGTAG	GATGCCTCTG	AGATAAGTCT	TCATGGTTAA	AAAAAAATCT
17751	GAATGTGAGT	GTTCCCTTAGC	CATTTAACAT	GTAACATATT	TATAGCTTCA
17801	CTGTTTTCTC	TTTTACCATT	TGGTGCTCTG	TTTTAAACTA	GATATCCCAC
17851	TTTGCTAGGG	AGGATAGAAG	CTTGTCTTGG	CAATGCCTAT	TTAGTTTCAT
17901	TGGTTATTAA	GAGGGGGAGA	TAAAAGATGA	AGAATAATGG	CCTCTCCAC
17951	TTTCTCTTTG	CACAAATGTA	TTTCTCTTCT	ATACTCCAAG	CCTCCCTGGA
18001	ACTCTCTTGG	GAGTGGTACT	CATGAAGGAG	ACAGGTTTGT	ATGTGTGGAG
18051	AGGAATCTGA	ATTAGCTCCT	TTATGATTGA	TGGTAAGGCC	ATTGCCTCAA
18101	GAAGCACACA	GGAAAGGCCC	ACCATCTTTC	CTTTGGCCAT	TGTTTCTTTG
18151	TTCTATTTTA	GCATGTAAGA	GCATCATGCC	CATATAATTT	CCTCTTAAAG
18201	TTGAATATTT	TGAATATATG	AAGGATTA AAA	AAATCAATAT	CTCTAACTTC
18251	TGTAAGATTA	ATCAAGCATT	CTTTGTATGC	TCATTTATAT	TATATATTAA
18301	ATTCCATATT	GATAGAAACT	CTTTTTTCTT	ATCTAGGTAT	TATTTTGCCA
18351	CATTTTATAA	AAATGCTTCT	CATGACAAAA	TTTTGAGTTA	CATTTCTTTT
18401	TGTTGGGAAT	GAACATAAAT	TACAAC TGAA	TATTAATGTC	TGGAATATAG
18451	CTTTATTCTT	ATTATTTTCC	TCTTTCTGTA	TAATTTGGCA	GACAAAGAAC
18501	CAGTGAAATT	TTAGAATAGT	TTAAATAAAT	CTCTGTAGGC	ATAGAACACA
18551	TTTTCATAAA	GAGGCTCATG	GTCAACAAAG	ATAAAATCAA	ATCATGACTT
18601	AGAAATAAAA	CTAAACTTCA	AAGGTAAAGT	ATTTGTTGGT	TTTATATTAG
18651	ATATACTGAT	ATTTTATTAC	AATTCCTAAC	CTCACAGATC	CCCCATTTCT
18701	TCCTCTTTCT	CTCCCCACCC	TTGTCACCTT	CCTTCCACTG	TAAAGGAAGA
18751	ACCAATGGCT	CCCAGGTTAT	CAGGAAACAG	GGCTGCTTGT	GTA CTATTCA
18801	CGATGCAGTT	AGCACCCACG	GGTTAAGTAG	GAAAAAAGA	AAAACATGAA
18851	CGGCATGCCT	CTTCCCTTGG	CTTCTACTTA	TCTTTTTCTG	CATGTGGAAT
18901	TTCCCTTGAT	TTTACCAGTG	ATATTTGGAT	TACTTTTCTG	TGCCTCCATT
18951	TTTTTAGTTG	TAGAATGAAA	ATAATAATAT	GATAAAGTGT	ACCTATTAAC
19001	TTCAATCCTA	TAAATACACA	TACACTATAT	GTGTGTATGT	GTGTGTGTGT
19051	GTGTGTATAA	TTTCTATCTT	TTTGCATGTT	ACCATGAAGA	CATTTCAGTG
19101	ACTACCAGGC	TATTCAGTGG	CTTTGTTTTG	TGTTCTCTCT	ATAGATCCTC
19151	GGTTGGTTTG	TACAGATTTT	TCTAGGACTA	AAACATATTC	ATGACAGGAA
19201	GATATTACAC	AGGGACATAA	AAGCTCAGGT	AACAGCTCAG	AGAGAAGACT
19251	AAGACAGAAC	TGATCTTTTCT	TTGAAGTACC	TCAAACAACA	TGACATTTTCT
19301	TCCATTTATA	GAACATTTTT	CTTAGCAAGA	ACGGAATGGT	GGCAAAGCTT
19351	GGGGACTTTG	GTATAGCAAG	AGTCCTGAAT	AAGTAAGTAC	TTTGAAAATA
19401	ATTTTTCTTT	CTAGTCAAAA	TAGCCCAAAT	ATGTATTTTT	AGATATCATG
19451	GATTAAGAAG	ATATTA AAT	CTTGTTGTC	TAAATAATTT	TAGGTAGCTT
19501	TATGTAAATG	CATTACATCA	GATGGTACTT	TGAGATTAAA	ATTCTCAAGA
19551	TAAATTGTGG	TGTAATAGAA	TGATGTTGCT	AATATTCTGT	AGTGTGATTC
19601	CAGTTTGTCA	AATATGGATG	TGACTGTAAT	ATGCATAAAG	CTAGAGAGAA
19651	TTTCGTGAAA	TAGGCAGGTT	TACACTTCTT	AATGAAAAAA	GTCAAACCTCT
19701	ATAAAAATATT	TGAAGAGATT	TATTCTGAGC	CAAATACGAG	TGACCAAAGG
19751	TCCATGCCTG	TGACATAGCC	CTCAGGAGAT	CCTAAGAACA	TGTACCCAAG
19801	GTGGCCGGTC	TACAACCTGG	TTTTGTACAT	TTTAGGGAGA	TGCAAGACAT
19851	CAATTAGATG	TACATGGGTT	TGGTCCAGAA	AAGCAGGACA	ACTCAAAGCT
19901	GGGAAGAATG	GGAGGGAGCT	TCCAGGTCAT	AGGTGGATTA	AAAAC TTTTCT
19951	TGATTGGCAA	TTGATTGAAA	GAGTCTATCT	GAAGACCTGG	AATTAGTGGA
20001	AGGGAGTGTC	TGGGTTAAGA	TAAGGGGTTG	TGGAAATGAA	GGTTTTTATT
20051	ATGCAGATGA	AATCTCCAAG	TAGCAGGCCT	CAGAGAGAAT	AGATTGTAAA
20101	TATTTCTCTT	TATCGGATTT	AAAAAGGTGC	CAGACTCTTA	GTTAACTTTT
20151	TCCTGGATCA	GGAAAAAGCC	TTGGAAAAAG	AAGGGAATTT	TCTTCAGAAT
20201	GTAGATTTTCT	CCCACAAGAG	ATACCTTTGC	AGGACTATTT	CAAGATATGG
20251	ACAAAGAAAC	ATGATTTGGG	GTA AATATT	TTGATTCCTT	TCAGGCCTGC

FIGURE 3G

20301	TATCTGTCAT	GTGATGTTAT	ACTAGAGTCA	GGCTGGACTT	TGGTATCTTA
20351	TTGCTACAAG	GAGTCTGCTT	TGTCAGTCTT	AAGGTCTGTT	TTAATGTTAA
20401	TGCTGGTCAA	CTGTGCCTGA	ATTCCAAAGG	GGAGGAGGAG	TTAATGAGGC
20451	ATATCAGACC	CTGCTTCCCA	TCATGGCCTG	AACTAGTTTT	TCAGGTTAAC
20501	TTTGGAATGT	CCTTGGCCAA	AGGGAGGGTT	TATGAGTTGG	TTGGGGGGCT
20551	TAGAATTTTA	TTTTTGTTTT	ACACACTTTC	TAGCAAAATA	AATTTGTGCA
20601	CCTGTTTGGA	AGACAATTTG	GTGGCAATAT	GTACCAAGAG	ATTTTTTAAAT
20651	ATCCTGTTTT	TGGGACTTCT	TCCAAGGGAA	TAATTTGAAA	TTTGGGAATA
20701	CGTAAATGCC	TAAATAAATTG	GGAAATGGTT	AAATTTAATA	AAGCTTGGCA
20751	TGGCCATGGC	CATGTACCTG	AATATATCAT	AAACATTTAT	GGTTTTGAAG
20801	ACTTCTTGAT	AACTTTGTTA	TACTAAGCAA	AGAAAATGGA	ATTCTGAATT
20851	TTAAATACAT	TGTGATCACG	GTTATATGAA	AAATATGTGT	GGAAAGAAGA
20901	CAGGAAGGAA	ATATATCAGA	ATTTTAACAA	TAGTTGTTTT	AGGTGCTAAG
20951	ATTCTGGGTA	ACTTTTTTCT	CCCTTATTCA	TTTTTGTTAT	TTCCAAGTTT
21001	TAAATCATGA	GGTTGCAATT	TGATAATCTC	TACATCTGAG	AGATTTTTAT
21051	AACATGACAA	TTTCATCTCT	TTGTGGAGTC	TTTAAGCCAT	AAAAAATATA
21101	TTTTAATGTG	TAAATTTTTG	GGAGGTGAAT	TGTAAGTTTA	AAAAATCAGCT
21151	GATTTAGTTA	GTTTTCAAC	ATACAGTGTT	TTGCTTTCTT	CTAACACATG
21201	TATGCATCAA	ATCTTGTTG	ATCCATTTTC	ACATTTTTTC	TTGCATGTCC
21251	ATGTCTTAAG	ACTTTTCTTA	CTCCAATAAA	AAATCATGCT	GATTTATTAT
21301	TTAATATAAT	TTACTAGTTC	CATGGAACCT	GCTCGAACCT	GTATTGGAAC
21351	ACCTTACTAC	CTGTCCCCAG	AGATCTGTCA	GAATAAACCC	TACAACAATA
21401	AAACGTAAGT	TGCTGACTCT	TAGTTTGAAA	GTGTCAGTAA	AATCTGATGG
21451	ATGACACTGA	ATGAAGATTC	CAGAAACTAA	AATTCAAATC	TCTTCTTTCT
21501	TTCTTATGGT	ACTTTTGTA	TTTCATTTGC	TTTCTGTGTG	AAATTGTTCT
21551	GGACCAAACCT	GAGGGTTGGG	TTGCTATTTT	TCGCGGTCCA	ATACGAGATG
21601	CAGATGAACCT	GGGGAGGAAG	AGAGTTTTTA	TTTCTGTAAC	CAGTACAGGG
21651	AGAAGGCCTG	GAAATTATCA	CCAGACCGAC	TCAAAATTAC	AAAGTTTTTC
21701	AGAGCTTATA	CACCTTCTAA	GCTATATGTC	TATGTGTAAG	TGTGCATTCA
21751	TTTAAAGACA	TACTGATTAA	CTCCTTTTAA	TCTATAACTA	AGGTCTGAGT
21801	CCTGAAGACT	TTCTTCTGGA	GCCTCAGTAA	GCTTACTTAA	TCTAAATGGG
21851	TCTAGGTCCT	GGGGTGATTA	CCCTTATTTT	GTCTCCTGCT	AAATCATGGA
21901	GGTTTAGGGA	GTTTCTGCAG	ACCTCCAATA	AACTTGTTTG	TGGAGGCCTG
21951	GGGAGTTTCT	TCAGACCACC	AATAAAACTT	GTTTAATCTT	AAAAGGCTCC
22001	TTGTTAAGAA	TTCTTTCATT	ATTTTGTGAT	GGTTTAAGGC	CCAGGAAAGG
22051	CCTAGGCAAA	ACTCTTGGTG	GGCTTTTGT	ACATTACAGC	CTTTGTATAA
22101	GGGCACTGGC	TTTTTTTTTT	TTATTTTTTG	AGATAGAGTC	TTGCTCTTGT
22151	CACCCAGGCT	AGAGTGCAAT	GGCACGATCT	CGGCTCACTG	CAACCTCCAC
22201	CTCCAGGTT	CAAGCGATTC	TCCTGCCTCA	GCCTCCTGAG	TATCTGGGAT
22251	TACAGGTGGC	TGCCACCATG	CCCAGCTAAA	GTTTTGTGTT	TTAGTAGAG
22301	ATGGAGTTTC	ACCATGTTGT	CCAGGCTGGT	CTCAAACCTC	TGACCTCACG
22351	ATCTGCCTGC	CTCAGCTCC	CAAAGTGTTG	AGATTACAGG	TGTGAGCCAC
22401	TGTGCCTGGC	TGGGCACTGG	CTTTTTAAGC	TTTTAATATT	TAACCTCACC
22451	ACTCAGTTAG	TATAGAAACA	GTTGTGATGG	AGGCCTGCAT	TGGTAAGACC
22501	TGGCCTGCCA	CAAAATGGGG	ATCCCAGTGA	CTATCTCTGA	GCAGTGTTAC
22551	CTGAAGGTTT	CAAACTTGTT	TAGAAGAAAG	CCATTTCTCT	TCATTTAAAG
22601	ATACAAGTGG	TATAAAAAAT	AACATCGAAA	ATTGCAGTCA	CTGTGATGTC
22651	CATTTTTGTA	TTATATGTTT	ATATCTTTGA	AGCACTGTTT	AGTCTATTGC
22701	AAGAAAGATT	GAAGAGGATG	AAGTAGAAGA	CAATGTGGTC	TGGTGACCGC
22751	TCACTGGATT	AGGAGCTAGG	AATCCTAGTC	TTGGCTCAGT	TGCTAACTTG
22801	ACCAAGTCAG	TTGACCTCTG	TGGGCTTCAG	TTCCCTAACT	CATAATAATG
22851	AGAGTATTGA	CTAGGTAATC	TTCAAGGTGT	CTTCCAGCTT	TAAAACCCAG
22901	TTAGTTTTTA	TGTATGTGAT	ATCAGAGTCT	GGTTCTCAGC	AATAATTTTT
22951	TTTTTTTTTG	AGATGGAGTC	TGGCTCTGTC	ATCCAGGCTG	GAGTGCAGTG
23001	GTGTGATCTC	GGCTCACTGC	AATCTCTGCC	TCCCAGGTTT	AAGCAATTCT
23051	CGTGCCTCAG	TCTCCCAAGT	ACCTGGGACT	GCAAGCACGC	CCCACCATGC
23101	CCAGCTAATA	TTTTGTATTT	TTAGTAGAGA	TGGGGTTTCA	CCATGTTGGT
23151	CGGGCTGGTC	TTGAATTCTT	GACCTCAGGT	GATCTGCCCC	CCTCAGCCTC

FIGURE 3H

23201	TCAAAGTGCT	GGGATTGCAG	GTGTGAGCCA	CCGCACCTGG	CCCTCAGCAG
23251	TAATGCTAAT	GTATACTGCA	AGAAAAAGGTG	AAGAGGAGCT	TTTGCTTCCT
23301	ATAAGGAGAA	GGAAAAAAT	TTCATTTTTT	AAAGCTGGCT	GCCATTGAAC
23351	AAGTTGGCGA	TAAGGAAGAT	TGAGTTCCCT	TTGGAAGTTA	ATTGTCCTTT
23401	TGTTTAGGAA	AAAATGCCCA	AGAGATACTT	GGCTATTGGA	CTTTGAAGGA
23451	GATAAATGGA	AGGCAAAGCT	CAGACAATAG	AGATTTACAA	AAAGAATAGT
23501	AAGAATTTCT	CTGCATAATA	AAATAACAGG	GATTTTTTTT	TTTTTTGAGA
23551	CATCCCCTGG	CACCAAGGAG	TTTGGCCTCA	AGTTAGTTGT	GCAGGAATTC
23601	AGGTAGGGTG	TGTTGGACGG	AAAGTAGGCT	GTTTCAGAGCA	GGGCATGCCA
23651	CAGACAGCCT	TGGGTCAGCT	GCATTGTTTT	GTTTGCTTGT	ACTGCTTTTC
23701	AAGAATTTGA	ATCAACATTT	AAATGCTGCT	GGATATGGTG	GCTCATGCCT
23751	ATAATCCCAG	CACTTTGGGA	GGCTGAGGGG	GATGATTGCT	TGAGTCCAGG
23801	GGTTCAAGAC	CAACCTGGAC	AACATTGTGA	GACCCTGTCA	CTACATCCAA
23851	AAAAAAATTA	AATATTGAAA	GACTTTAAAA	TATGCATAGT	TTGTACCTCT
23901	GAAAATTGGA	AGATCTTAGC	AATAATCAGG	TGGGTAGCCG	CTGGCTCCAT
23951	TAGAGGACTG	GTTCACCACA	GTCCTCAATA	TGCAGAGTGG	TCTCAGGCCT
24001	GCAACTGGCC	CCACCCAACC	CCCAGGTGGC	TGCAGTACTG	CCTGAGCCCT
24051	GGGGGCATAT	GAATTCTCTG	CCCTGGCTGC	AGAGGGTCCT	CTGGGAACAG
24101	AAGAGAAATT	TGGGTCTGTG	GAAGCCCTAG	TAAAGACAAA	AGTCTGTGTG
24151	GTGTGAAATG	GTCAGTGAGT	TTCTAGAAGG	TCTAGAAAGT	TCATGTTTGT
24201	TTCTTGGGTC	AGGTGCAGGC	GGCTCACACC	TGTAATCCCA	GCACTTTGGG
24251	AGGCCAAGAA	GGGAGTATTG	CTTGAGCTCA	AGAGTTTGAG	ACCAGCCTGA
24301	GCAACATGGT	GAAACCTTGT	TAATGAAAAA	AAAAATTATT	AAAAAAAATC
24351	CCACAAATTT	GTTTCCCACC	AATCTTACCG	TCTATTGTAC	TTACTACCAT
24401	CTTTTGTACT	CAAACTTTTA	GTATGAGTCT	ATCTCTCTCT	CCTTCTCTCT
24451	GACACACACA	CACACACACA	CACACACACA	CACACACTCA	TGCACAAAGC
24501	ATTGCTGCTA	GAGGAGCCAT	TTACCTCACT	CCTCACTTTA	ATGATTCCCT
24551	CTTGCTTTGA	CTCCTTGACT	TCTGATTAGA	CATTTTTTGA	TCTTTTAGAT
24601	TTAATTGTGC	TTTTTGTCT	ATAAAATAAC	TCCTCAAACC	AATCACATAT
24651	AAATATTTAT	GAAGTACTAA	ATCTGTAAGG	AGCAAAGCTC	ATGATATATA
24701	TTTTAAGTAT	ATTTTTAAAT	GTTTATTGAG	AATCAGATAC	TATGTTTATC
24751	ACATAATATA	ACTTTGGTTC	TGTCAAAAGC	CTTGAGTAGG	ATATATCTTT
24801	CAAAATCAAC	CAAATATTAC	CTTTTGAGTC	AAAACAAATC	CATGTTTGAG
24851	TTCTGCCTGC	CTCCTCCAAA	TTGCTCAACA	TTTCATCATA	CATACATTGT
24901	TTTTGAGCAG	GAAGCTGAAC	TAAATATTAA	GCCACCAGGT	TGTAGCAAAG
24951	TTTGTGTGCC	TTTCTTTGAC	TAGAAATCTG	ACAAACTACA	AATGGTTTTT
25001	ATTTTACCTC	TTATCTTCTA	ATAAGAATTG	ATGATATATC	TGAAAGCATT
25051	TGTAAAAAGCT	GATCAACTTA	CATAAAATTG	TAAAGCGACA	CAAATTTAAG
25101	GCACTGTAAG	GATAAAAGCT	TTTATTAAGA	ATTATGGATA	TTTTCTTGGC
25151	ATGTAAACTC	TTATCTTCTT	TAGGGATATT	TGGTCTCTTG	GCTGTGTCTT
25201	ATATGAGCTC	TGCACACTTA	AACATCCTGT	AAGTATGCTC	ATTGTCAGAC
25251	TAATCTTGAA	TTATTGGAAT	TGTAGAAAAG	AAATTAACTT	CTGGGAGAAA
25301	AAGGTTAATG	TTTGTTTTTA	TTAGATTGTT	AAAAATTATA	TGGATAAGCT
25351	ACTTAAAAATA	ATGATAGATG	ACATGGAAAG	CTGTCCAAGC	AATATTATAA
25401	AGTAAAAAGT	CCAAGTTGGA	GAATAGTATG	TGTAGCATAT	TTCCATTAAA
25451	AATAAATTGT	GTGGGCTTGG	CGTGGTGGCT	CATGCCTGTA	ATCCCAGCAC
25501	TTTGGGAGGC	TGAGGCGGGT	GGATCACTTG	AGGTCAGGAG	TTGGAGACCA
25551	ACCTGGCCAA	CATGATGGTG	ACACCCCGTC	TCTACTAAAA	ATACAAAAAT
25601	TAGCCAGGCA	TGGTGGCATG	TGCCTGCAGT	CCCAGCTAGT	TGGGAGGCTG
25651	AGGCACGAGA	ATTGCTAGAA	CCCAGGAGGC	AGAGGCTGCA	GTCAGCTGAG
25701	ATTGCGCCAC	TGCACTCCAG	CCTGGGTGAC	AGCGAGACTC	CATCTAAAAA
25751	AAATAATTAA	TTAATTAATT	ACTGTATGAA	TAGATACGTT	CAGCAAAAGA
25801	AAAATGTACA	TGGGCAAAGT	TCATAGGAAA	CCAGGCACAA	GCTTTTAAGA
25851	GTCTTTTCCC	AGAGGTCAACA	TGGGATGTGC	CAAATCCTCC	AGCATTGTTA
25901	CCCACGTCAC	CTGTGAAATG	TGATCTATAA	GAAAGCTCAT	CGGATATACC
25951	CAGTGCCCA	GATTTTACT	GGGGACTGGT	CACATAGGCA	CCCTCTACCT
26001	GGCATATGCC	AAACTTCCAG	ACTCCTGGAA	AGAAAGCCCG	TGTTTCAGCAT
26051	AAACCATTTT	GTTACATAAA	ATAGCTGAGG	CAAAGATAGC	CACTCTTGAC

FIGURE 3I

26101	ATTCAGGGAA	TGGTGGGAAT	TCTTCTGAAA	TCTTAGTTCC	CAGACACCAG
26151	CCACGGGCCA	ACATTGTAAG	CAGGCCTTTC	TGAGGAGAGC	TTGCTACATC
26201	AACTCTTTTC	TCCACAGCTG	TCATCATTGT	TATTAATTAT	TGTCAAGGGT
26251	TGCACAGCCA	GTGCTGACC	AAAATGTGTA	CTCCATTGTT	TTTTTGAGAT
26301	GGAGTCCCGC	TCTGTTGCCC	AGACTGGAGT	GCGGTGGCAC	GATCTCAGCT
26351	CACTGCAACC	TCTGACTCCT	GGGTACAAGC	AATTCTCTTG	CCTCAGCCTC
26401	CCGAGGAGCT	GGGATTACAG	GCACCCACCA	CCACACCCGG	CTAATTTTTT
26451	TGTATTTTTA	GTAGAGTCAG	GGTTTTGCCA	TGTTGGCCAG	GTTGGTCTTG
26501	AACTCTGAC	CTTGGGTGAT	CTGCCCACCT	TGGCCTCCCA	GAGTGCTGGG
26551	ATTACAGGCG	TGAGCCACCA	TGCCCCGCCA	ATGTGTACCT	TTATTGCTAC
26601	ACCATGGAGT	TGAATATTAT	TATGTATAAA	TAACTATTGG	TTTCATACAA
26651	TAGAAGATTT	CTGGTCTATG	AAGCATTTTA	GAGGAAATTA	AACGATGTTT
26701	ATGTTAATTT	TAAAAAGCAA	GAGATAAAAT	TTCATATCAA	TATGACCTCA
26751	ACTTTGTAAA	ATAAACATCA	TTTTTAAAAG	AGATCAGAAG	GAGCTATACC
26801	TCTGAGTGGT	AAAATTATAC	ATATTTTCCC	CTGTCTTTAT	AACTTCCTAT
26851	ACCTTCCAGT	TTTTTTATTA	TGAGTAAACA	TTATTTTGAT	AATAAGACAG
26901	AATTA AAAACA	AAATAAAAAAC	TTGTTTTTAAA	TAACATGGCA	TCTTGTTGAA
26951	TAACCTCAGT	ATCTGCTCAT	GAAAGATTAG	TTGATGAAAA	CAATTTAAGG
27001	TGGACCAAGT	TGCTTCTTTT	TTATTTTTTG	ATTGAGACAG	GGTCTCACTC
27051	TGTCACCCAG	GCTGGAGTGC	AGTGACGCAA	TCACGGCTTA	CTGCAGCTTT
27101	GACCGCCTGG	GCTTAGACAA	TCCTCTTGCC	TCAGCCTCCC	AAGTAGCTGG
27151	GACCACAGGC	TCATGCCACC	AAGCCCAGCA	AATGTTTTAA	AACCATGATT
27201	TGGAGAGATG	AGGTCTAACT	ATGTTTCCCA	GGCTGGTCTT	GAACCTCTGG
27251	GCTCAAGTGA	TCCTCCTGCC	TTGGCCTCCC	AAATTGCTGG	GATTACAGGT
27301	GACCCTAGTG	CTTCTAACTA	CAATTTAAAA	ACATTGTTTT	GCTTCTTGGT
27351	ATATTTGTTA	CTTTAAACACT	TTTATTATTT	GTTACTTTAG	TAACTTTTCT
27401	CTGATTTAGT	GTCATTTCTC	CTTGTCCTTT	CAGTTTGAGG	GTAACAACTT
27451	ACAGCAGCTG	GTTCTGAAGA	TTTGTCGAAG	ACATTTTGCC	CCAATATCTC
27501	CGGGGTTTTT	TCGTGAGCTC	CATTCCCTGA	TATCTCAGCT	CTTTCAAGTA
27551	TCTCCTCGAG	ACCGACCATC	CATAAATTCC	ATTTTGAAAA	GGCCCTTTTT
27601	AGAGAATCTT	ATTCCCAAAT	ATTTGACTCC	TGAGGTAAGT	TTTGAGGTGA
27651	CTGTTTGGAT	TTTGGCAGAG	ATTTTGGGTT	GCAGGTCCTT	GACACGTGTG
27701	TTCGGTTTTA	GGTCATTGAG	GAAGAATTCA	GTCACATGCT	TATATGCAGA
27751	GCAGGAGCGC	CAGCTTCTCG	ACATGCTGGG	AAGGTGGTCC	AGAGTAAGTG
27801	TGACTTTGGC	ATGCAATCAA	AAGTATTTAT	TACACATGTC	TCACACAGAG
27851	AGTAATGCAA	GGAAATTTCA	CCAAACATAT	TGAAAGTGGA	CATTTTAAAA
27901	AATACAAGCA	GTATAAGCAG	GAGAAAAATC	ATCTTGTCAA	ATGGCAACTA
27951	GTGAGTGTGC	CTGAAAAGTTG	TATATCTAGC	TCATGCATGA	CCTGCAGGGT
28001	TCCTTCTCGT	TAGTCAGGAA	ACCTCCATGA	AGCAGAGGAC	ATGCTAATAG
28051	AGATGCTTGA	AGAGGTTGAG	CCCAAACCTA	ACTTTTGTGT	AGTGAAGGGA
28101	CAGAGTGGGA	GAAGGTTGCA	GATAGACATG	GATGATGAGA	TGAAACTTAT
28151	TTTTCTAAAA	GAGGATAGAC	TGGCAATTAA	GAATTCTGTT	GCAAAGGACC
28201	ATTGGAGCTG	AAGTTAGGAT	CTTGGGGCCT	AATTGATAAC	AGTAAGAAGT
28251	GTTACTTTGT	GGTTCCCAAA	GAAGGCAGGA	GATATTTTAT	GGTAGTAATA
28301	AATACAGAAA	ACTTTTTTTT	TTTTCCGAGA	CGGAGTCTCG	CTCTGTCGCC
28351	CAGGCTGGAG	TGCAATGGCG	CGATCTCTGC	TCAGTGCAAA	CTCCACCTCC
28401	CGGGTTCATG	CCATTCTCCT	GCCTCAGCCT	CCCGAGTAGC	TGGGACTACA
28451	GCCGCCCATC	ACCACTCCCG	GCTAATTTTT	TGTATTTTTT	TAGTAGAGAC
28501	GAGGTTTCAC	TGTGTTAGCT	AGGATGGTCT	CGATCTCCGG	ACCTCGTGAT
28551	CCGCCCGCCT	CTGCCTCCCA	AAGTGCTGGG	ATTACAGGCG	TGAGCCACCG
28601	CGCCAGGCCG	GAGAAAACTA	TTTTAGTCCT	GGTGTCAAGA	ATCAGCTAAG
28651	CTGTGTGTCA	GAGGGAGGGG	TACGTTAAGA	AAGAGAAAAA	TACTAATTCA
28701	TTTGATGCTG	TGAAAGTCAA	AGCCCCAGAA	TTTAGCTGTA	ACTGAATGCC
28751	TGGACTTACA	ATATCAGGAG	GAGCAGAAAG	CCTCTCAAAG	GAATCCATGA
28801	CAGGGAAATG	TTATCCATTG	AGACAGAGAT	TCTAAAAATCA	AGGAAAGTTA
28851	AAGAGAAAGT	GAATGAGCCT	CTTTGCCATT	TAATTTGACT	AACATTGTTG
28901	TATACCAGTC	TAGATTGAGA	ATGTTTAGAA	AATAGACAAG	TACAGAGTAT
28951	GGGACTGTGT	ATTGTCCATA	TTTCTAATCT	AGGTAAGATA	GGAGAACAAG

FIGURE 3J

29001	AACAATTTTT	TTTTTATTGA	GATGGGGTCT	CACTGTGTTG	CCCAGGCTGG
29051	TCTCGAACTC	CTGAGCTCAA	ACAATCCTCC	TACCTTGGCC	TCCCAAATTG
29101	CTGGGATTAC	AGGTGCGAGC	CACCTTACTC	AGCCCAAGAA	CAAATTTTGA
29151	TGGAGATAAA	GACAAGCATT	AGAAGATCTA	CTCATACCTC	AGTCCTGGCA
29201	CTTTGGGAGG	CCAAGGAGGG	CAGGTCACCG	GAGGCCAGGA	GTTTGATGCC
29251	AGTCTGGCCA	ACATGGCCAA	ACCATGTCTT	TACTAAAAAT	ACAAAAATTA
29301	GCTGGACCTG	GTGGCCCATG	CCTGTAATCC	CAGCTCCTTG	GGTGGCTGAG
29351	GCACAAGAA	CGCATGAACT	CGGGAGGTGA	AGGTTGCAGT	GAGCTCAGAC
29401	CCTGCCACTG	CACCGTAGCC	CGGGTGACAG	AGTGAGACTG	TCTCAACAAA
29451	AAAAAAAGAG	AGAAGATCTA	CTCATAAATT	CCAAACAATG	TGGCATGAAT
29501	GGAGTGGCCT	GATAACCCAA	GCTCTAATGA	CCAAATTTAA	TAACTTTTAT
29551	TATTACCCCA	TACATATTGT	TTCTGTAAAT	GTAAATATTA	ATTTCTATTT
29601	TTCTGAAAAA	AAGTGATGTT	ATATATTACT	AGAAATATGC	AAAGGGACTC
29651	TGAAAAAATG	GTTTTTTTCA	TTTAAAGAAA	TTGCATATTA	ATTTTTTCATC
29701	AGTACTCTCA	CTGTGTGTAA	AATATCTCTG	GCTAAAAAGT	AAACTTACTG
29751	TGTTATGAAA	TGTAGCTTAT	GTTTATACTC	TTACAAGTAT	CAGTATTAAT
29801	GGTGTAACA	TTTTAAAAAA	TTGAAGCTGT	TTTATTTTGG	TTAATTAAGA
29851	GTGTAATAA	CAAAAAAGTGA	GATTCCAGGG	AAAGTGCCCA	CCAAGATCAA
29901	GGATATCTGT	GCCAATTAAA	AGGAATGCTA	TATTGCATAG	AAATGAATGG
29951	AGACCACCAG	CTGGAGCCCA	GAAGGCCAGA	TCTGTAAGTC	ATTCTAAACC
30001	CTCCTTTGTG	TTTTTTTAGCT	ATGGTATATG	CTTTTTGTTT	GTTTGTTTGT
30051	TTGTTTTGAG	ACGGAGTCTC	GCTCTGTGCG	CAGGCTGGAG	TGCAGTGGCG
30101	CGATCTCGGC	TCACCGCAAA	CTCCACCTCC	CGGGTTCAAG	CAATTCTTCT
30151	GCCCCAGCCT	CCTGAGTAGC	TGGGACTACA	GACGTGTGCC	ACTATGCCCA
30201	GCTAATTTTT	GTATTTTTTG	TAGAGATGGG	GTTTCACCAT	ATTGGCCAGA
30251	ATGGTCTCCA	TCTCTTGACC	TCGTGATCCA	CCTGCCTGGG	CCTCCCCAAG
30301	TGCTGGGATT	ACAGGTGTGA	GCCATGGCGC	CCGGCCCCGG	CTAATTTTTA
30351	TACTTTTAGT	AGAGACAGGG	TTTCACCATG	TTGGTCAGAC	TGGTCTCGAA
30401	CTCCTGACCT	TGCGATCAGC	CTGCCTCGGC	CTCCCAAAGT	GCTGGTATTA
30451	CAAGCATAAG	CCACTGCACC	CAGCTGTTAT	ATTCTTTTTT	TTTAATTTTT
30501	TAATTAATAA	AAAAATTTTT	GTGGGTACAT	AGTAAGTGTA	TATATTTATG
30551	GGGTATATGA	GATGTTTTGA	TACAGGCAAG	CAATGTGAAA	TAAGCACATC
30601	ATGGAGAATA	GGGTGTTTGT	CCCCTCAAGT	ATTTATCCTT	TGAGTTACAA
30651	ACAACCCAGT	TATACTCTGT	AACTTATTTT	AAAATGTACA	ATTAAGTTAC
30701	TATTGACCAT	AGGCAGTCTA	TTGTGCTATC	AAATAGTAGG	TCTTATTCAT
30751	TCTTTTGTFT	TTTTAACCCA	TAAAGCTATG	GTATATTCTG	ACAGACCTAT
30801	CTGCACATGT	TCATGAGGTA	CAAGCTTATT	GTTTGGAGTC	CACAAATTTT
30851	GTACTTAAAA	TGAAGTATTC	TGTACTGAGC	ATTATAATGG	TATTTTGTTG
30901	GACAACTTCT	AGTTTTTATA	TTTTATGAAA	CAATGCTGTA	TGCTCTTATA
30951	AGTATACTTT	AGGCTTAATT	TTCTTTTTAT	AACTGAAATT	CTTCTAATTT
31001	CTAATAAATA	AGATTTTTCT	GTATAGGAAA	AGTGAGTAAC	ATAGCAACAG
31051	AAAACACTCT	GCATTTAATA	TTCTTAATTC	TAACATATTA	TGTATAGGAT
31101	TGAGAAGTTT	TTATGATATA	ATAATTGATA	TTTCCCTAGT	GATTCTTTGT
31151	GTTTAATTAT	TTGAATTCAC	TTCAGCAGAG	TGTTGAATCT	TTTAGGTCAT
31201	ACTAGTGAAG	TGCTTCTGGT	ATGTAAATGA	TAAAATGGCT	ACTGTCTTTT
31251	AATTAAGAG	TTGTATTTTT	AAAGAAGGCT	CATGGTTAAA	TTAAGAACCA
31301	TTTGGAAGTG	TATTTACTAA	GTGTTTACTT	GATATATAGA	CATTTTAGAA
31351	AATGTGTTGG	TATATAAACA	TTTTTTTTAAA	AACCGATTGT	TTAAGTTATT
31401	GCCCTTCATT	TGATAAAGGG	CTTTATTTAT	TTATTTATTT	ATTTATTTAT
31451	TTATTTATTT	ATTTATTTGA	AAGAGGGTCC	TGCTGTGTCA	CCCAGGCTAG
31501	AGGGCAGTGG	CATGTCTCAG	CTCACTGCAG	CCTGGATGTA	TTAGTCTGTT
31551	CTCATACTAC	TATAAAGAAC	TGCTTGAGAC	TGGGTAGTTG	ATAAAGACAA
31601	GAGGTTTAAT	TGGCTTACAG	TTCTGCAGGC	TGTACAGGAT	GCATTGCTGG
31651	GGAGGCCGCA	GGAAACTTAT	AATCATGGCA	GAAGGGGAAG	CAGGCTCATC
31701	TTAAATGGCC	AGAGCAGGAG	AAAGAGAGCA	AAGGGGGAGG	TGCTACACAC
31751	TTGTAAACAA	CCAGATCTCT	GGAGAACCTA	CTATCACAA	AACAGTAAGA
31801	GGGAAATCTG	TCCCCATAAT	CTAATCACCT	TCCACCAGGC	CCCTCCTCCA
31851	ACATCAGGGA	TTACAATTCA	ACATGAAATT	TGGGCAGGGA	CACAAATCCA

FIGURE 3K

31901	AACCATATCA	TTCCACCTTT	GGCCCCTCCC	AATTCCCATA	TCCTTCTCAC
31951	ATTGCAAAAT	ACAATTATCC	CTTCTCAACA	GTCCCCCAAG	GCTTAACTCA
32001	TTTCAGCATT	AACTCAAAAG	TCCACAATTC	AAGGTCTCTC	TGAGACAAGT
32051	CAAGTCCCTT	CCACCTGTGA	GGCTGTAAAA	TAAAAAACAA	GTTAGTTACT
32101	TCCAAAATAC	AATGAGGGTA	CAGGCATTGG	GTAAATACAC	CCATTTCAAA
32151	AGGGAGAAAT	CAGCCAAAAC	AAAGGGTTTA	TAGACCCCAT	GCAAATTCAA
32201	AACCTAGCAG	GGCAGTCATT	AAATCTTAAA	GCTCCAAATT	CCTTTGACCC
32251	CATGTCTCAC	ATCCAGGGCA	TACTGGTGTG	AGGAGTGGGC	TCTCAAGGCC
32301	TTGGGCAGCT	CTGCTCCTGA	GGCTTTGCAG	GCTACAGCCC	CTGCGGCTGC
32351	TCTCACAGGC	TGCTGTTGAG	TGTCTGCGGC	TTTTCCAGGT	GCGTGGTGCA
32401	AGCTGTCGTT	CAATCTACCG	TTTTTGGAGT	CAGGAGAATG	GTGGCCCTCT
32451	TCTCACAGCT	CCACTAAGCA	GTGCCCCAGT	GGGGACTCTG	TGTGGAGGCT
32501	CCAATGCCAC	ATTTCCCTC	TGCACTGCCC	TAGTAGAGGG	TCCCCCTGAA
32551	ACAGGCTTCT	GCCTGGACGA	CTAGGCTTTT	CCATACATCT	TCTGAGATCT
32601	TGGTGGAGGC	TCCCACGCCT	CAACTCTTGC	ACTCTGTGCA	TCTGCAGACT
32651	TAACACCATG	TGGAAGCCAC	CAAGATTTAC	GGCTTGCACC	CTCTGAAGCA
32701	ATGGCCTGAG	CTGTACCTTG	GGCCGTTTTA	ACCATGGCTG	GAGCTGGAGC
32751	AGCCACAATA	CAGGACACCA	TGTCCTGAGG	CTGCACAGAG	CAGTGGGGCC
32801	CTGGGCTTGG	TCCTCAAAGC	CATTCTTCCC	TCCTAGGCCT	CTGGGCCTGT
32851	GATGAGAGGG	GCTGCCTCAA	AGGTCTCTGA	AATGCCTTCA	AGGCATTTCC
32901	CCCATTATCT	TGGCTAACAA	CATTTGACTC	CTCTTTATTT	TTGAAAATTT
32951	CTGCAGCTGG	TTTGAATTGC	TCCCCAGAAA	ATGGGTTTTT	CTTTCTAGGC
33001	TGCAAACTT	CTTAACTTTT	ACACTCTGCT	TCTCTTTTAA	GTATAAGCTC
33051	TGGTTTTACA	TCATTTATTT	GCTCACAAAT	ATGACCATAG	GGTGCTAGAG
33101	CAGCCAGGCC	ACATCTTGAA	TACTTTGTTG	CTTAGAAATT	TTTTCTGTCA
33151	GACGCCTTAA	ATCATCACTC	TCAAAGTTCA	AAGTTCCACA	GATCCCCCTAG
33201	GGTAGTGGCA	CAATGCCTCC	AACCTCTTTG	CTAATTCATA	ACAAAAGTGT
33251	CCTTTGCTGC	ATTTCTCAAT	AAGTTCCTCA	TCTCCATCTG	AGACCTCCTT
33301	AGCCTGGACT	TTATTGACCA	TATCACTATC	AGCATTTTGG	TCACTATGAT
33351	TTTAAGAAGT	CTCTAGGGCA	TTCCAAACTT	TCCATCATCT	TCCTATCTTC
33401	TTCTGAGCCC	TCCACGCTCT	TCCAACCTCC	GCCCCATTACC	CAGTTCACAA
33451	GTCACTTTCA	CATTTTCAGG	TATCTTTATA	CAATACCCCA	CTCCTGGTAT
33501	CAATGTACTG	TGTTAGTCCA	TTCTCATACT	GCTATAAAGA	ACACCTGAGA
33551	CTGGGTAATT	TATAAAGAAA	ATACATTTAA	TTGGCTCACA	GTTCTGCAGG
33601	CTGTACAGGA	AGTATGGCTG	GGGAGGCCTC	AGGAAATTTA	TAATCATAGC
33651	AGAAGGGGAG	GCAGGCTCAT	CTTACATGCA	GGAGGAAAAG	AGTGAAGGGG
33701	TAGCCGCTAC	AAACTTTTGA	ACAACCAGAT	CTCATGAAAA	CTCACTCACT
33751	ATCACAAGAA	CAGCAAGGGG	GGAATCTGCC	CCAACGATCC	ATTTACCAGG
33801	CCTCGTCTCC	CAACATTGGG	GATTACAGTG	CAACATGAGA	TTGGGCAGAG
33851	ACACAAATCC	AAAGCATATC	ACTCGACCTC	CCAGGCTGAG	ACACAAATCC
33901	AAAGCATATC	ACTCGACCTC	CCAGGCTCAA	GTGATCCTAC	CGTCTCAGCC
33951	TCCTGAATAG	CTATACTACC	GGTATGCACC	ATGATGCCCA	GCTAGTTTTT
34001	ACTTTTTGTA	GAGTCAGGGT	CTCACTGTGT	TGCCCAGGCT	GTTCTTGAAT
34051	TCCTGGGCTC	TAGTGATATG	CCCGCCTCAG	CCTCCCAAAG	TGCTGGGATT
34101	ATAGGCGTGA	GCCACTGTGC	CCAGCCTAAG	GGCTTAATTT	TATTAAGAA
34151	ATAAGAAAAG	TATGTTGTGA	TTTCAAGGAC	TCTTTATCAG	ACCTGTAGAA
34201	GGGAAAACAC	ATCTAAAAGA	TTTGAGGATG	AATTAAATTA	CGAACTGTTG
34251	AACACGCTGA	CATTTTTCCA	GTTCTTGAA	AAGGTAAAAAT	TGATTTCCAC
34301	AGGAACTACC	TCTGATATTC	CTATTACTGT	TGGGATGTTA	GAGAACATTT
34351	TAAAGAAAAT	GTTTTATTGCC	TTTCAATACT	TTTCTATATT	TTTTACCACT
34401	TTTCAACAAG	TCATTAGTAG	CATTTTCTTC	TAGGTTGTAT	ATAGGTGAAA
34451	TTGTAAAACA	AAGAAAACCTA	CTTCTTGTTT	TAAAAGATTT	TAAAAATAGG
34501	CAGGTGCAGT	GGCTCACGCC	TATAATCCAA	CACTTTGGGA	GGCTGAGGCA
34551	GGAGGATCAT	TTTCAAGCCAG	GAGTTCGAGA	CCAGCCTGGT	CAACACATTG
34601	AGACCCACCC	TCTACAAAAA	GTAATAATTAA	AAAAAAATTT	TTTTGTTTTT
34651	TACTGGACAC	AGTAGCATGT	GCCTGTAGTC	CCAGTTACTT	GGGAGGATGA
34701	GGCAGGAGAT	CCCTGGATCC	CAGGAGTTTG	AAGCTGCGAT	GAGCTATGAT
34751	CACACCACAG	TCCTGCAGGC	TGGGTGACAG	AGTGAGATCC	TGTCTCAGAA

FIGURE 3L

34801	TTTAAAAAGA	AAAGAAAATA	TTTTAAAAAT	AAACATATAA	TTTGTATTTA
34851	GATTAATGAA	CTAAATTTTA	TACATTTTACT	TAAATATTTA	AATAGAACTA
34901	TATGAAAGTG	CCATTTTTCT	AGATTAATTA	TGGTCAATTC	TGGGCAATTT
34951	CTTTTTTTGA	GACGGAGTCT	CACTCTGTCA	CCCAGGCTGG	AGTGCAGTGG
35001	TACGATCTTG	GCTCACTGCA	AGCTCCGCCT	CCCAGGTTTG	TGCCATTCTC
35051	CCGAGTAGCT	GGGACTATAG	GCACCCGCCA	TCACGCCCAG	CTAATTTTGT
35101	TTTTGTGTTT	TTAGTAGAGA	CGGGGTTTCA	CCTTGTTAGC	CATGGTGGTC
35151	TCGATCTCCT	GACCTCGTGA	TCCGCCTGCC	TCAGCCTCCC	AAAGTTCTGG
35201	GATTACAGGC	ATGAGCCACT	GCGCCAGCC	AATTATGTGC	AATTTTCATAT
35251	GGTCCAATCT	AACATATATG	TGAACCATAT	AGCAGTAAAA	ACAACAAAGA
35301	ATATAACATG	TTACCTCTTT	ACATGAGGAC	ATTTTGTTT	TAATTGTTCT
35351	TGTTATTCAT	ATCCCAACT	ATTAGTTCCT	AGGTCTTTCC	AGTAGTTTTA
35401	TCTTTTTTTC	TCTTTTTATT	ATTAAGTGA	AACTGTAAAC	TAGACAGAGT
35451	TGCCACGCTT	TAGGTTAAAT	TGACCCCACT	TTGCTCTTTA	GCAAGAAGGT
35501	CTTGACTGGC	TTTTATATCT	TAATTTGATC	TGTTTCTTGT	CTTCTAGCTC
35551	AGTGGCTTCT	ACTCAGTTGG	AAGATAAACT	GTCATTTCTG	GTTCTCCTAT
35601	TCTCATTCTG	TTCTGGTTGG	GAAGGGTGGT	GAGGGCTGGG	ATGGTGATAT
35651	GCCCATCATG	GCTGTTATAT	GACCTTTTTT	AATATTTTCT	CTGGAAGAAT
35701	GATTCTGATT	CAGCATCTTC	TTTCCTTTAA	GTCATGATGC	CATTTTGCAT
35751	TTAGTCAATT	TATCAGAAAC	TAAAAATGTT	GCAAATCCCC	ATATGTGTGA
35801	GTTTCACTAT	GCTTTTTATT	TCCCTGTAAA	GTATGGTAAG	GTATAAATGA
35851	GTTTATGAAA	AATAGAAAAC	AATAATTCTG	AGTTTAGTTT	TGGATCTTGG
35901	GTTGCCTGGG	CATACTCACT	AGCTAAGTAT	TTTTCACATA	CTAGCCATGA
35951	AGTATGCATG	ATTCATATCC	ATACCTTAGC	AAAATTGTAA	ACCACTATAC
36001	TATCTAGTAC	TTAGGTCTTT	TTGTACTCTA	GGATTTGGGG	ACTCTTAAGA
36051	TTATTCTGGA	AAAAAAAGTA	TAGAAGAAAA	ACAGCAAAAA	TACACCTTCA
36101	GTGCCTTATC	TTAGCTATGG	TCACTGTTAT	ATTGTCAAGT	ATTATAAATT
36151	TGTATTATGG	TTTTTTTTTT	TGAGATGGAG	TCTCGCTCAC	ATTGTGCAGG
36201	TTGGAGTGCA	GTGGCATGAT	CTCAGCTCAC	TGCAACCTCC	ACCTCCTGGG
36251	TTCAAGTGAT	TCTCCTTCCT	CAGCCTCCCA	AGTAGCTGGG	ATTACAGGCG
36301	TGCGCCACCA	TGCCTGGATA	ATTTTTGTAT	TTTTAGTACA	GACGAGGTTT
36351	TGCCATGTTG	GCCAGGCTGG	TCTTGAACCT	CTGACCTCAG	GTGATCCACC
36401	CGCCTCAGCC	TCCCAAAGTG	CTAGGGTTAC	AGGTGTGAGC	CACTGCACCC
36451	AGCCTGTATT	ATGGTTTTTA	AAAACATCCC	CTCTTGTTTT	CTTCAGATAA
36501	AAATGATAGA	AAGACCCAAA	ATTGCTGCTG	TCTGTGGACA	TTATGATTAT
36551	TATTATGCTC	AACTTGATAT	GCTGAGGAGG	AGAGCCCACA	AACCAAGTTA
36601	TACCCCTATT	CCTCAAGAAA	ATACTGGAGT	TGAGGATTAC	GGTCAGGAAA
36651	CGAGGCTATG	TCCATCCCCA	AGTCAATGGT	AATATTGTGG	TCTAGCTTAA
36701	GCTTTGGTTA	ATCTAAAAAT	ATCTTTATAT	ATTAACATTT	ATTATTCTGA
36751	AATCCAAATT	CTCCTAACAC	AAATAATCCA	AGAAGAACTT	TCCAAATCTT
36801	CATTTTAAAC	ACATAGTTCC	CTTGACCTTT	TTCTTTTGTT	TGCTTTTGTA
36851	GACAGTCTCA	CTCTGATGCC	TAGGCTAGAG	TGCGGTGGCG	CAATCTCAGC
36901	TCAGTGCAAC	CTCTGCCTTC	TGAGTTCAAG	CGATTCTCGT	GCCTCGGCCT
36951	CTCCAGTAGC	TGGGACTACA	GGCGTGCACC	ACCATGCCCA	ACTGATTTTT
37001	ATATTTTTAG	TAAAGACAGG	GTTTCACCAT	GTTGGCCAAC	CTGATCTTGA
37051	ACTCCTGACC	TCAGGTGATC	TGCCCGCCTC	AGCCTCCCAA	AGTGCTGGGA
37101	TTACAGGCAT	GAGCCACCAT	GCCTGGCCAT	GTTAGTCCCT	TCTTTCTATG
37151	TCAGCCCTAT	ACCTGCTTGT	TAGTTGGTTC	TTCAAATTCT	CAGGTACCCT
37201	CTCACCAGGC	AGCCACTGAC	CTCATGTGAT	CCACCTGCCT	TGGCCTCCTA
37251	AAGTGCTGGG	ACTACAGGCA	AGAGCCACTA	TTCCAGCCT	TTCTTTCTTT
37301	TTTTTTTGT	AGAAAGATT	TGTTTTTATT	TCCATCAGAA	TGTCATATAT
37351	GTTACACAAA	TCAAATCTGT	TGACATCTCA	AGCTTATAAC	AATTACGTGT
37401	TCTTATAAAT	TACGTGGGAA	TTACATGTAC	TGTGAGAAGT	GTTGTAATTA
37451	TGATGTAATG	TATATTATAA	TTTAGCCTAC	AGAAGTAACA	AAGTCTTGTA
37501	ATTAAATAAA	GCAATAAATG	TGTTGATAGA	TTATTACAAT	TGATAAGTAA
37551	TTGATAAATT	ATCTTCTTTT	TCCTGTAACC	CTTCTTCATC	TCAAGTCTGA
37601	TCTAGCTTAT	TTTCTTATTC	ATAGAGCTGC	TTAACTGTAG	GCACAGACCC
37651	ATACCCTTGC	TCTTTTAATA	TTCTTTCTTC	CTCCTACTAA	ATTCCACTAT

FIGURE 3M

37701	ATGGCAGGTG	AAAAAATAGT	TGTGTATATT	TCATTTCTCA	AAGAGGTTAC
37751	TAATATGAAT	CAATAATTGA	ATCATTAATA	TCAAATGATC	ATTTGAGACA
37801	TTTTGAGAAA	TAAGATATAT	TTCATTCGGC	ATTTATGTTT	TAGGGATTTT
37851	CAAAATATGG	ACATGTTAGA	AAGAAAATAG	TATTCCTAAA	TTGGTCTTAT
37901	GGTAGATTTT	CAAAAAATTT	ACTCCATAAT	AGATTTCTGC	AGATCTACAA
37951	TATTTTCAAA	TTTTTTTCAC	ACTGATGTTG	ACATTCCTGT	GTTCAGAATA
38001	ATTGACACCT	AACAGAGGCC	TGAAGACTTA	AGTCTAAGAG	TTCTATTTTA
38051	AAAATGTTTT	GTCATCAATT	TTTTTGTTC	AGGGTTAAGA	ATTTGTTACT
38101	TTGGCGACTC	TGATTGTTTA	TTGTTGAAAT	TTTGGATGAA	TTATGAAAAA
38151	CACAAGATAC	TATGGGATGG	CAATCTCATT	AATAGTGAAA	ATGAGATAAG
38201	CAAGAATGAT	AAGAGAATAA	TTTCTTCAGA	AACATATAAC	GGGAAAAGCA
38251	TATGTTTTAT	CTTTAAAGAT	ATTGGGCACT	GTTGTGGTTT	TTATCGATCT
38301	TCATAACACA	TTTTTAATTA	TCTCCACAAT	TATCAAAAGT	TATGTCTTCT
38351	GTCCGTTCAA	ATTGTAATAT	CCATATTGGA	CTCAATTAGT	GAGGGACATA
38401	GATTTTACAG	AAGAACTGGA	GCAGCCACAA	AACTCCCTTT	CTCTTTTCTC
38451	AACCACTGGG	AAAATATATC	TTCCACTCTT	TGTCTAGATT	TGAGAGCTGT
38501	CAAGCTATCA	ATTATTTTGA	CCACATGTGA	TTTTATATCT	CCCAAGCTCT
38551	CACATGAAAC	AGTAGGAAGG	GTCCTTCTCT	TTCTGGATG	CCCCTTTGAT
38601	GCCTGGTAAC	CCCTCCTCTT	TGTATACTCC	CTCATCCCCA	GCTTTCTGTC
38651	TGCTGGAGGT	CCAATTACAG	GCCATGGGAT	GGAGGAAAAG	GATTTTTTTT
38701	TTTTTTTGAGA	CAGAGTCTCG	CTCTGTCGCC	CAGGCTGGAG	TGCAGTGACG
38751	CGATCTTGGC	TCACTGCAAG	CTCCGCCCCC	TGGGTTTACA	CCATTCTECT
38801	GCCTCAGTCT	CCAGAGTAGC	TGGGACTACA	GGCGCCTGCC	ACGACACCTG
38851	GTTAATTTTT	TTGTATTTTT	AGAAGAGACA	GGGTTTCACT	GTGTCAGCCA
38901	GGAGGGTCTC	AATCTCCTGA	CCTTGTGATC	CACCCGCCTC	GGCCTCCCAA
38951	AGTGCTGGCA	TTACAGGCAT	GAGCCACCAT	GCCCGGCCGA	GGAGAGGAA
39001	TTGTATAGG	ATTTGGGGGG	TGGAGAGGGA	ATAGGTAGAC	AGAGAGATAG
39051	AGAAATGCTT	TTGGACAGCC	CCTGGGTGTT	GGAATCATTT	TTCTCATGAA
39101	GATATTGATA	CATGTGCCAG	TTAGGCTTAT	GAGACAGATG	AGTGCTACAA
39151	TTTACCCTCA	TTTGATTCAA	GAACATCTG	TGTGTCAGGC	ACTTCACAGC
39201	CCTAATCTCT	TCTAATCCTC	GTATCAATTC	CTGTGAAATG	GTACCATGCC
39251	CACTTTACAG	CTGAGGAAT	AAGACTCAAA	GACTTTAGCT	TGTCATTTCA
39301	TCCTATTTCT	AAATCCCTGA	TTATTAACCT	GCCTCTTTGT	AAATTGGGGA
39351	TGCTTATCAT	GATGTTCCCT	CCTAAAGGAG	TTATTTCTGA	AATTACAGTT
39401	CTGTCTTTGG	AGCCTTAGAA	GTTACTCGTA	TTCCAAAAAA	CTTATGGTCT
39451	GAAATGCGGT	TTTTATTTAG	CAACCAATAA	TTACAGAAAT	GTTTTACAGG
39501	AAATTCTGCC	AAAAAAAAGA	TACATAAAAT	GTGAGTATAA	ACTTGAAAAT
39551	TGTTTGACTG	GAATTGACTA	AAATTGTGCT	GGAAAAATAC	CTTAAACATT
39601	TGGAGAGACA	GCTAAACCAT	TATTTCTTTC	CTCATTAAGC	ATTTATGTGC
39651	GGAGATAAAG	GGATGGATGG	AGGGACACAT	TCTGCTCTCA	GGGAGCTCAG
39701	TATGTGGTGC	AGGAAACAGA	TATGCAGCCA	TTCTTTTTTT	TCTTTTCTTT
39751	TCTTTTTTTC	TTTTTTTTTT	GAGATGGAGT	CTCACTCTGT	CACTCAGGCT
39801	GGAGTGCAGT	GGTGCGATTT	TGGCTTACTG	CAACCTCTGC	CTCCCTGCTC
39851	AGCCTCCCCA	GTAGCTGGGA	TTACAGGTGC	CCACCACCAC	GCCCCACTAA
39901	TTTTTTTTTAG	CAGAGACGGG	GTTTCACCAT	GTTGGCCAGG	CTGATCTCGA
39951	ACTCCTGACC	TCGTGATCCA	CCCACCTCGG	CCTCCCAAAG	TGCTGGGGTT
40001	ACAGGTGTGA	GCCACCACAT	CTAGCCACTA	TTGTTAAATC	AGGAGCGACA
40051	ACCTGTACAT	TAGACACCTA	CACAAAGCGT	GAGAACTTCT	GGGTGTGGGT
40101	CTGTTTTCT	CCCCACAACA	TATTATAGAG	AATGGAAGGA	CTGAATCTTG
40151	TCCTGAAGAA	AAATCACTGG	ATAAGAATAT	TTTTCTGTTT	AATCCTCTCC
40201	TGTATCCCCA	CTTGTTACTC	TTCATCCTTT	TTTCCTTTTG	ATTCCAAAAT
40251	TTTCTTTTCC	AATGTAAAAG	TTCTGTAAC	GTGAACACT	TCTTGAACTT
40301	GGAACCTCAA	GCCACTGGTG	AATTGTGAAT	CTCATTAATA	AACTGAAAAT
40351	TACTCGTCAA	ATTGGTGCCT	AAGATTTCGT	CAAGTTTCTA	CTTAAGCTGA
40401	ACATTCTTAT	TTTCTAAGGC	CTGCTGAGTA	CCTTCAGAGA	AAATTTGAAG
40451	CTCAACAATA	TAAGTTGAAA	GTGGAGAAGC	AATTGGTAAG	TAAAAACCA
40501	AATATGGGAA	GCAATTAGGA	ATTTCTTAAT	AGTTTTTCTG	TTACACAGATT
40551	TTCAAGTCAA	AGTTCATTCC	ACCAGAAGGT	CAAGAATACT	CTCTACTAGT

FIGURE 3N

40601	CCCCAGTTTT	TTTTGTTTTT	GTTTTTGTTG	TGTTGTTGT	TGTTGTTTTC
40651	TGAGACAGAG	TCTCGCTCTG	TCACCAGGCT	GGAGTGCACT	GGTGTGATCT
40701	TGGCTCACTG	CAACCTCTGC	CTCCCAGGTT	CAAGCAATTC	TCCTTCCCCA
40751	GCCTCCTGAG	TAGCTGGGAT	TACAGGCGCC	CACCACCACG	CCCAGCTAAC
40801	TTCTGTATTT	TTAGTAGAGA	CAGGGTTTCA	CCATGTTGTC	CAGGCTGGTC
40851	TCGAACTCCT	GATCTCGGGT	GATCCACCCA	CCTAGGCCTC	CCAAAGTGCT
40901	GGGGTTACAG	ACGTGAGCCA	CTGCACCTGG	CCCCAGTCCC	CAGTTTTTAA
40951	TAGCTAAATA	AAATAATGGG	AACAGGCTTG	AATCACCCCC	TTAGCAGTCC
41001	GGTTTCTTCC	TTGGCTCTAT	CTCTTCTGTG	GGACCTTGGA	CAGTTCATTTC
41051	AGCCTATCTG	AGCCTTAATT	TCCTTTTCTA	TAAATGACAA	TTTTTAGAGT
41101	AGATGAGCTT	CAAATTTCTT	TGCAGTGCTG	TAGTGCTTTG	GTTCTATTTT
41151	GTTAAAGATT	CTGCTGCACA	TTAAAAAAAG	TGACAAGGGG	CCAGGTGCGG
41201	TGGCTCATGC	CTGTAATCCC	AGCACTTTGG	GAGGCCAAGG	TGGGCGGATC
41251	ATAAGATCAG	GAGTTCAAGA	TGAGCCTGAC	CAACATGGTG	AAAGCCCGTC
41301	TCTACTAAAA	ATACAAAAAT	TAGCCAGGCA	TGATGGTGCA	CACCTGTAAT
41351	CCCAGCTACT	TGGGAGGCTG	AGGCAGGAGA	ATTACTTGAA	CCCAGGAGGA
41401	GGAGGTTGCA	GTGAGCCGAG	ATCGCCCTAC	TGCACTCTAG	CCTGGGCGAC
41451	AGAACGAGAC	TCTGTCTCAA	AAAAAACAAA	AAAAACAAAA	ACCAACAACA
41501	AAAAAGTGAT	TAGGCCAGAT	ATTATGGCTC	ATGCCTGTAA	TCCCAGCACT
41551	TTGGGAGGCT	GAGGTGGGTG	GATTGCTTGA	GCCCAGGAGT	TCGAGACTAG
41601	CCTAGGCAAC	ATAATGAGAC	CTTATCTCTA	CCAAAAAATA	CAAAAAATTAC
41651	CCAGGTGTTG	TGGTGTGTGC	CTGTAGTCCC	AGCTACTGAG	GGGGCTGAGG
41701	CCGGAGGATT	GCTTAAGCTT	GGGAGGCAAA	GGTTACAGTG	AGCTAAGATT
41751	GCGCCACTGT	ACTCCAGCCT	GGGTGACAGA	GTGAGACTCT	GTCTTAAAAA
41801	AAAAAAAAAA	AAGAAAGGCT	GGGCTTGATG	GCTCATGCCT	GTAATCCCAG
41851	CACCTTGGGA	GGCCAAGGCG	GGCAGATCAC	GAGGTCAGGA	GATTGAGACC
41901	ATCCTGGCTA	ACACAGTGAA	ACCCTGTCTC	TACTGAAAAA	ACAAAAAATT
41951	AGCCGGGTGT	GGTGGCGGGT	GCCTGTAGTC	CCAGTACTC	GGAAGGCTGA
42001	GACAGGACAA	TTGCTTGAGC	CTAGGAGTTG	GAGGCTGCAG	TGAGCCAAGA
42051	TCATGCCGCT	GTACTCCAGC	CTGGGTGACA	GAGTGAGACG	CTCTCAAACA
42101	GAAAAAAATA	TATATTTTTT	AATGCTTTAT	AATTAAGAAA	ATTCTACTAC
42151	TTACCACAAA	AAAAACTCCC	AAATACTGAG	TTTGCTTAGT	GATATAATTC
42201	TTATTTATAG	GAAAAAGTCA	ATGTCAAATC	AGAAGATGTT	TCCGAAATCA
42251	AAGTATGCAT	TATAAATTAT	TTCATTCAAT	AAATAGGGTC	TTCGTCCATC
42301	TTCTGCCGAG	CCAAATTACA	ACCAGAGACA	AGAGCTAAGA	AGTAATGGAG
42351	AAGAGCCTAG	ATTCCAGGAG	CTGCCATTTA	GGAAAAACGA	AATGAAGGAA
42401	CAGGTTAAAA	ACTGTTTAAT	TCCAGGGCTA	CCCTTGATT	TCTTTGTATT
42451	ACTGCTTTTT	GTACTGTAAT	AGGGAGTTAC	TTCTATTTCC	TACAGTGCCC
42501	CTGAATATGT	CAACACCATG	CTGAGTGTTA	TAGGGGATAC	AGAGTTAGGT
42551	ATTTCACTTT	CTCAGATAAT	GCGATATGGC	TAAGTTCATA	AAGCTTTTCA
42601	CCTTGAGATT	CATAGAGTAA	CTGTCCATCA	GTAACAGGTT	TGGGATTTGT
42651	ATTAGTTTTCC	TGGCTGTCTG	TAACAGAGTT	CAACAACTA	GGTGGCTTAA
42701	CACAATAGAA	ATGTATTGTC	TCACAATTCT	GGAAGAGTGG	AAATAGAAAA
42751	TCAAGGTGTC	AGCAGGACCA	AGTGCCCTCT	GAAACCTGTA	GGGGAATCCT
42801	TCCTTGCCCTC	TTCTAGCTT	CTGGTGCGTC	ACTGGCAATC	TTTGGCATTT
42851	CTTTACTTGC	AGTCGCATCA	CTCCATTCTC	TGCCTTCATC	ACATGCTGTT
42901	CTTCCTGTGT	GTCCCTGTCT	TCACATGGCC	ATCTTCTTGC	AAGGACATCA
42951	GTCATATTGA	ACTAAGGGCC	CACTGGTATG	ATCTCATCTT	AAGTAGTCTC
43001	ATCTGCAGCG	ACCCTGTTTT	CAAATGGGGT	CACATTCTAA	GGCACTGGGG
43051	GTTAGGACTT	CAACATATCT	CTTTTTGGGG	AGGAACAAAC	TTCAGTGCACT
43101	AAGAGGGTTA	TATATAAAAG	TGGGATTTAT	AAAGTAAGTG	TACATCATGA
43151	ACACATTTGG	GTTATATATA	AAATTGAGCT	CTGTAGCTAA	AGCCACTGTC
43201	TCACAGGGAG	TGAAGTACTG	CAGCCAAAAC	ATAAGGCAGA	TTATCATCTT
43251	TAGGAGCAAC	ATATTTTTCT	AACCTTATTT	TATATTACAC	ACTTTTGAAA
43301	TTGTAGGCTG	CAGAAAGATT	ATTTTTGTGA	TGGTGTTTCT	AAACATTTAA
43351	AGTTCTGCGA	TTGGGTTTGC	TTTCCAGGAA	TATTGGAAGC	AGTTAGAGGA
43401	AATACGCCAA	CAGTACCACA	ATGACATGAA	AGAAATTAGA	AAGAAAGATGG
43451	GGAGAGAACC	AGAGGTAAAT	TCATTCTTCT	AGGGGAAACA	TTGTTCTATC

FIGURE 30

43501	GATTTAGAGC	TAACTAAATT	GAGCTGGTAT	TAAAAGTAAT	GATTCCTTA
43551	TAGAAAAGAT	AAAGTTTTAT	CATAGAGATA	ATCATGTAGA	CTTCTTTTTT
43601	AATAGGAAAG	CTGTCAGACC	TCATTGGAGC	TTCAGTTTAT	TATGGTTTAT
43651	GAGAGACTAC	ACAAGATAAT	AAGGATATCT	GAGATTCTCA	GGAATGGCTA
43701	TTATTAAAAG	TACTTATTGA	TTGTTTCCTT	CATGAATCAC	TCAATACATA
43751	TTTATTGAGT	GGCAACTTTA	GACAAGAGCT	GGATTAGATG	CAGAAAGTCC
43801	AAAATGAGTG	TAAGTTCATG	CCCAGAAGGT	GGGAAAAAAA	CAAAACCAAC
43851	ACACTAGCAT	TTTTTCAACT	CTCTGCAGGG	TAAGGTTCTA	AAGGCTATTT
43901	AAGGCCAAAAT	CTGAGTGCAG	TTGAACTGAT	TCTTAAAAAT	CTCTTAAAGG
43951	CGCCACATTG	GAAATTCATC	CTTCCATCTC	CCAAGAAGGT	CTCTAGAGTT
44001	GGCACAGATC	ACTGCTTCTT	CAGAAGAGCT	TCACATGAAA	TAGCCAGCCT
44051	GTGTTTGGAA	ACCATGTTGT	AAGAAAGACA	CATGGCTATT	GAAACACTAG
44101	GAACACACTC	AGTGCCCTGG	AATGCTCTCC	TAGGAGAAGC	TTGCAGGCAC
44151	TGAGACAGCT	GTCTCCCATC	CCACATGCAC	TTGGCCACAC	ACTCATTGAG
44201	TAGAGCTACC	ATGCTGCTGA	AATTGATCTC	TCTCTCTCTT	TCTCCCACCG
44251	CAGTGCATAC	AGATAAATTC	ATATAAGTCA	AATGAATGTA	TGGTGCAATT
44301	CAGTTGTGTT	TGCCAGGCCA	TGAACTAGAG	CTTTCACATA	CTGTATTAGT
44351	CTGCTCTCAT	ACTGCTAATA	AAGACATACC	CAAGACTGGG	TAATTTATAA
44401	AGAAAAAGAG	GTGTAATAGA	CGCACAGTTT	CACATGGCTG	GGGAGGCCTC
44451	ACAATCATGG	CAGAAGGCAA	AGGAGGAGCA	AAGTCATGCC	TTACATGAAG
44501	GCAGGCAAGA	GAGCTTGTGT	AGGGGAACTC	CTATTTACAA	AACCATCAGA
44551	TCTTGTGAGA	CTTACTCACT	ACCATTAATA	TAGTATGGGA	GAAACACCCC
44601	CGATGATTCA	GTTATCTCCA	CCTGGCCCCA	CCCTTGACAA	ATGAGGATTA
44651	TTACAATTCA	AGGTGAGATT	TGGGTGGGGA	TACAGAGCCA	AACCATATCA
44701	CGTTCATACT	TTCTTTTATT	TACCCCTGTA	CAGAGAAAGT	AAGTAGCTCA
44751	TCCAAAGTCA	CGTAGCTATT	ACAAGGCAGA	CGAAATATTT	AAATATCTGA
44801	CTCTAGGCTG	GGCACGGTAG	CTCATGCCTG	TAATCCCAGC	AATTTGAAAG
44851	GCTGAGGTGG	GAGGATTGCT	TGAGCCTAGG	AGTTTGAGAC	CAGCCTGGGC
44901	AACATAGGGA	AACCCTAGCT	CTAAACACAC	ACACACACAC	ACACACACAC
44951	ACACACACAC	ACACACACAC	ACACACACAC	TCTCTCTCTC	TCTCTCTCTC
45001	TCTCTCACTC	TCTCTCTCTC	TCTCTCTCTC	TTTAAATTAG	CCGGACATGG
45051	TGGTTTGCAC	CTGTAGTCCT	AGCTACTTGG	GAGGCTAAAG	CAGAAGGATT
45101	GCTTGAGCTA	GGAGCTAAAG	GCTGCAGTGA	GCCATGATTG	TGCCACTGTA
45151	CCCCAGCCTG	GGATACAGAG	CAAGACTCGG	TCTCAAAAAA	ATAAAGTAAA
45201	ATAAAATGAA	AATCTGACTC	TAAAACCCCT	ACTCATGTTC	ATGCCTGTAA
45251	TCCTAGCATT	TTGGGAGGCC	AAGGCAGAAG	GATCGCTTGA	GCCCAGGAGT
45301	TTGAGAGCCG	CCTGGGCAAC	ATAATGAGAC	TCCATATGTA	CAAAAAATTT
45351	AAAAAATTAG	TGGGTCAATG	TGGCAAATGC	TTGTAGTCCC	AGCTACTCAG
45401	GAGGCTGAGT	TGGGAGGCTG	AGGTTGAAGC	TGCTGTGAAC	TGTGATTTTT
45451	CCACTGCACT	CCAGCCTGGG	CAACAGAGGG	AGGCCCTGTC	CCAAAAAATA
45501	AAAAAATACA	ATTATAACCA	CTATTCTTTC	TGGCATATGC	AGTTCTACTT
45551	ATAAATGGTT	GGAATGACGA	GACACATGTA	TAAAACAATC	ATAGAGTAAG
45601	CCCTGTAGGT	GCACAGGAGC	CAAGATGAGC	AGAATGAGCA	GGTAGCGGGT
45651	ATTTATGGAA	GAAGTGGGTG	GGGCCTAAAG	AGTGGAATTT	GGAGAGGCAG
45701	AGTTAAAGGA	GGAGAGTGGG	CATTCTGAAA	GAACCATGCA	AAGGTTGGGA
45751	CAGAGGACTG	TGTGTGCTGG	GAGGGGCAGC	CTGGAGGTTG	TTCTCTCTGG
45801	AGCAGAGGCC	TGGCTCATGG	GCAGCCTGGA	GCCATCATCA	GCCTTATGTC
45851	TAAGGCTGAT	CTGGGATGGG	CAGCCTGAGC	CCTGCAAAAA	TGGATAGCAG
45901	ACATTGGTCA	GGCGCGGTAG	CTCACGCCTG	TAATCCCCAG	CACTTTGGGA
45951	GGCTGAGGTG	GGCGGATCAC	GAGGTCGGGA	GATCGAGATC	ATCCTGGCTA
46001	ACACAGTGAA	ACCCTGTCTC	TACTAAAAAG	CCAAAAAATT	AGCCAGGCGT
46051	GGTGGTGCGT	GCCTATAGTC	CCAGCTACTT	GGGAGGCTAA	GGCAGGAGAA
46101	TGGCATGAAC	TCAGGAGGCA	GAGCTTGCAG	TGAGCCAAGA	TCGCACCACT
46151	GCACTCCAGC	CTGGGTGACA	GAGTGAGACT	CCATCTCAAA	AAAAAAAAAAA
46201	TGGTGGATAT	CAGACATTTT	TACAGAGGCT	ATGGAGGAAG	GATTTGGGAA
46251	ATACTGAAGC	TGTGGCGGGG	AAAAGGAGCT	ATAAAAAGGG	TTCTGTCCAG
46301	CCATTTTCATC	ATTGATCGCG	CATCAGCCAA	GTAGCCTTCA	GAGCTCACTC
46351	AGAACCAATC	TTGTTGACTG	TGTATAATTT	GTGTTAAAGG	AGAACTCAAA

FIGURE 3P

46401	AATAAGTCAT	AAAACCTATT	TGGTGAAGAA	GAGTAACCTG	CCTGTCCATC
46451	AAGATGCATC	TGAGGGAGAA	GCACCTGTGC	AGGTAATGAT	GGCTATGATC
46501	AGATGTGTGT	GCTTGCACTG	TGTGTGCTCT	ACCCCAAGTG	GCTCTTACCC
46551	TTCTCTGTGC	AGCAGAACCA	CGTAGGGAAC	TTTTTTTTTT	TTTCTATGAG
46601	ACGGAGTCTC	ACTCTGTCGC	CAGGTTGGAG	TGCAGTCGTG	CGATCTTGGC
46651	TCACTGCAGT	GTCTGCCTCC	TGGGTTCAAG	TGATTTCCCTG	CTTCAGGCTC
46701	CCGAGTAGCT	GGGACTACAG	GCATGCGCCA	CCATGCCCAG	CTAATTTTTG
46751	TATTTTTAGT	AGAGACAGGA	TTTCACCATG	TTGGCCAGGA	TGGTCTTTAT
46801	CTCTTGACCT	CGTGATCCAC	CAGCCTCGGC	CTCCTAAAAAT	GCTGGGATTA
46851	TAGGCATGAG	CCACCGCCTT	TTTACCAGAA	CTTTTAAAAA	CTCAGATGCC
46901	TCTCTCTGCC	CCAGATGGTC	TGGGATGAGG	CCCAGGCATT	CTGTCTGCAG
46951	AAGCTTGCTG	GGTGATTTAG	TAAGCAGCCA	AGTTTGAGAA	CTGCTGCTAT
47001	TTAGTATAAG	AACGTTCCAC	TCTCTGGAGG	TCTCTAAGTCA	GTGTATCAGA
47051	CACATTGGTC	AGGAAATCTG	AGTCAAGTTC	TCTTCCATTT	CAACCTTATG
47101	TTTTTGGTGG	AGGTAAGAGC	CTGGGCAGAG	TTGAAATAAC	AAATAAATCT
47151	CAAGAGAGTT	TTTTTCCCTT	CTGAGAAAAG	ATAATGCAAT	TATAATACAA
47201	GATGAATCTG	TTGATTTCAA	CCAATTCTGA	GAATTATTAA	ACCTGTGAAA
47251	TGACCTGATA	AACAATGCTT	TTATGGTTAC	ATAAAAATAAT	TACATAAAAT
47301	GTTTTACTTT	CCAAGGAGTT	ATATTTATTT	TGCGAATAAG	AAGCCCAAGT
47351	GTGCTTTTAT	TTTTGCTTAG	TAAGAAGATT	CTCAATGATT	TGGCCCATAC
47401	TAAGAATTAT	TATTATCTTT	TTTTTTTAGA	TGGAATTTTCG	CTCTTGTTGC
47451	CCAGGCTGGA	GTGCAATGGC	ACGATCTTGG	CTCACCGCAA	CCTCCGCCTC
47501	CCAGGTTCAA	GCGATTCTCC	TGCCTCAGCC	TCCTGAGTAG	CTGGAATTAT
47551	AGGCGCCTGC	CACCGCGCCC	AGCTAATTTT	TGTATTTTAG	TAGAGACAGG
47601	GTCTCACCAT	GTTGGCCAGG	CTGGTCTTGA	ACTCCTGACC	TCGGGTGATC
47651	CACCTGCCTC	AGCCTCCCAA	AGTGCTGGGA	TTATAGGCAT	GAGCCACCCC
47701	GCCTGAGCGA	ATTATTATTA	TCTTTATAAT	TAGAGTAATT	CTCTGTGTTT
47751	TAAATTATAT	TTATTATTAG	AGCTTGGTCC	AGAGTCAACT	AGAAATGGAA
47801	AATCCTCAAG	GTATTATAAA	CTTGTCATTT	AAAGGTGCCA	GTAGGATCAC
47851	AGTCACATTC	CATAAAAAACA	CGGCTCAGAT	GTTACAGACA	TGTTTTTCTC
47901	TCACATTTTT	TAACCTGGTT	AGAGTAAATC	CAGTGCCTTA	AAGTTTTTAA
47951	TAAGTCAGGT	AATTAATAAT	AAACCACTGG	AAGCCTCAAA	AAGTTTGTAT
48001	CAGGAATTGG	GTGAATAAAA	TCTTGTATAT	TTTATGCAAG	AGGAGTAACT
48051	TTGAAAGAAA	ACACACCAAA	ATGCCAATGG	TGGTAATTGG	TGGTATCTGG
48101	ATTGGTGTGA	GTAGGAATGA	TTATTGTCTC	TCTACTTTTT	AGATTTTTTA
48151	TAAGAAGGTT	ACAGAACTTT	TACTACAAAT	ATGTATAATA	AAGTATCCGT
48201	TCTTAGTTC	TGTCAGCACT	CTAATCAATA	TCTTCAAACA	AAAAAGCCAT
48251	CTGAAAGACA	GAAATGGTGG	CACGAGACTA	TAGTTCCAGC	TATTTAGGAG
48301	GCCGAGGATC	CCTTGAGCTC	AGGAGTTTGA	GACCAGCCTT	GGTAATATAG
48351	TGAGACCCCA	TCTCTAAAAA	AAAAGAAAAG	GCATCTGATA	TTTCCTGAAG
48401	GCTCCTCCAG	AGCAATCCAG	CAGCAGATAC	CTTTGCAAAC	TTTTGTAAAG
48451	GAAATAATTA	TCACTTAATT	TGTCTAATTT	TTGGATTTAG	GTTTTAATTA
48501	TCTTTTTTGA	AGGGAATATG	CAGCTATATA	ATAAGACACT	TTAAAAAAGT
48551	CTCTACTTGT	AGAGTTATCT	TTCCAAAATA	CTGATTTGAA	CATTATTTCT
48601	CTACACGACA	ATCAATGGCG	ACTGCCATTT	CTCTTAGCAT	GGCATGCTAG
48651	ACTTTTGTGA	GTTGTTCCCTA	ACAGAATGTT	CCAGCCTCAT	TGCTCACATT
48701	TCCCCCAAAC	ATACCCAAAG	CTCTAAATGT	CTCAGATTAC	CTTTTTTTTT
48751	TTTAAATGAC	ATATTTTTTA	TTTCTTTAAG	TGATTTTTTT	CACTGTGGTA
48801	AAATACATAT	AACATCGCCT	TTACCACCCT	AACCATTTTT	TTTTTTTTTT
48851	TTAATTGATC	ATTCTTGGGT	GTTTCTCGCA	GAGGGGTATT	TGGCAGGGTC
48901	ATAGGACAAC	AGTGGAGGGA	AGGTCAGCAG	ACAAACAAGT	GAACAAAGGT
48951	CTCTGGTTTT	CCTAGGCAGA	GGACCCTGCG	GCCTTCCGCA	GTGTTTGTGT
49001	CCCTGGGTAC	TTGAGATTAG	GGAGTGGTGA	TGACTCTTAA	CGAGCATGCT
49051	GCCTTCAAGC	ATCTGTTTAA	CAAAGCACAT	CTTGCAACGC	CCTTAATCCA
49101	TTTAACCCTG	AGTGGACACA	GCACATGTTT	CAGAGGGCAC	AGGGTTGGGG
49151	GTAAGGTCAC	AGATCAANNN	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN
49201	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN
49251	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN

FIGURE 3Q

49301	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN
49351	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN
49401	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN
49451	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN
49501	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN
49551	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN
49601	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN
49651	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN
49701	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN
49751	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN
49801	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN
49851	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN
49901	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN
49951	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN
50001	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN
50051	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN
50101	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN
50151	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN
50201	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN
50251	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN
50301	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN
50351	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN
50401	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN
50451	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN
50501	NTACGAAAAC	CAGTCAGGCG	TGGCGGTGCG	CCCCTGCAAT	CGCAGGCACT
50551	CGGCAGGCTG	AGGCAGGAGA	ATCAGGCAGG	GAAGTTGCAG	TGAGCCGAGA
50601	TGGCAGCAGT	ACAGTCCAGC	TTCCGGCTCGG	CATCAGAGGG	AGACCGTGGA
50651	AAGAGGGGAG	AGGGAGAGGG	AGAGGGAGAG	GGAGAGGGAT	CAGATTACTT
50701	TTTAAAGCCC	TACTTATTTA	AAAAGACATC	TTCTTTTAA	CCTCCAGGCT
50751	TTTGTAAAAT	GCTTATTTCT	CTACTGAAAT	ATCCCTTCCC	TCTCTTCTCT
50801	TCTTGCAGAA	CACATCTATC	AGACCTCCTG	GTGAAGTTTC	TAGCACAGCT
50851	TTTTTCTCTT	TCTCCCTTAG	AATTAATAAC	TGCCTCATCT	GTATTTCCAC
50901	AGCATTTCCA	AGTACTTCAT	ACACCAGCCT	GTGTCAGTTT	GAAGCATTAT
50951	TAGCTATTTG	CCCTGCAAAC	TTGGGAAGGG	TTTTTCTGCC	TTGCAGTAGT
51001	ATGAAGTCTG	AAATCAGGAC	TATGACTTAT	CTATCTTACT	TATATTTGTG
51051	AAAGTTGGTTG	TCTGATTTGC	TTGGATAGTC	TGGTCATCTC	AATTGTACAA
51101	TAGTGCTCC	ATTACTTTAC	TTTCCTTAA	ATACAACGAT	CTCAGATTCC
51151	AACCCCAATC	TACTCCAGTG	GGTGGGACAT	TCAACCTTAG	TGTGCTGTCA
51201	AGCTCTCCAG	GGTCATGTCA	TCTGAAAGGC	CCTCTTGGCC	CTGTGAAGAC
51251	TGATTAAGTG	TGTAGCCATG	GAGTCTGGGA	TCTTGAGGCA	GGAAGTCTAG
51301	GCTGGTGTGC	AGTCTCTTGC	TCACTACTCC	AATGTACTGC	CACAGATTAG
51351	GACTTGAGTC	CGCCATCTCT	TTAAAAAATA	AAACAGTTTT	ATTGAGATAT
51401	AATTGATCAT	AATAAACAC	ACATATTTAA	TGTATATACT	TTATAAAATT
51451	TGGCAGGCAC	ACCCATGAAA	CCCATCACCA	CAATCAATAT	AGTGAACATA
51501	TCCATCACCT	GCAAAAGTTT	GTTGCGCCCT	TTTGTAAACT	CCTCTCTCTT
51551	ATTCTCCCTA	CCTCTCCTCC	CATCTCATCC	CCATGCAATC	ACGGATCTGC
51601	TTTCTGTGCG	TGTAGGTTGG	TTTGAATTTT	CTAGATTTGT	TTGGATTACA
51651	TAAATGGAGT	CGTGCTGTAT	GTGCTCTTTT	TTCTGGCTAC	TTTCATTAC
51701	ATAATAATGT	TGAGATTTAT	CTATGTTGCA	CATATTAATA	GTTCATTATT
51751	ATTCTTTATT	GCTGAGTATA	TTCTATTGTA	TGAATGTATC	AAAATTTATT
51801	GATCCATTCA	CTGTAGATGG	ATATTTGGGT	TGTCTCCAGC	TTTTGGCTAT
51851	TATAAATAAA	GCTGCTAGGA	ACATTCATAT	ACAAATCTTT	TTTTTTTTTT
51901	TTGAGACAAG	TTTCGCCCTT	GTTGCCCAGG	CTGGAGTGCA	ATGGCACAAT
51951	CTCAGTTCAC	CACAACCTCT	GCCTGCTGGA	TTCAAGTGAT	TCTTCTGCCT
52001	CAGCCTCCCA	AGTAGCTGGG	ATTACAGGCA	TGCGCCACCA	CGCCTGACTA
52051	ATTTTGTATT	TTTAATAGAG	ACAGGTTTTC	ACCATGTTGG	TCAGGCTGGT
52101	CTCGAAGTCC	CGACCTGAGG	TGATCCACCC	ACCTCAGCCT	CCCAAAGTGC
52151	TGGGATTACA	GGTGTGAGCC	ACTGTGCCTG	GCTATCATGT	ACAAATCTTT

FIGURE 3R

52201	ATGTGGTCAT	GTGCTTCTTT	TCTTTCTTTT	GGGTAAATAC	ATTGGACTGG
52251	GATGGATGGA	TCATATAGTA	GGTGTATATT	TAACTTTCAG	AGAACTACCA
52301	AATGGTGTTT	CAGAATGGTC	GCACTGTGTT	ACACTCCCCT	TGACATTGTA
52351	TGAGTGTTTC	AGTTCTCTCT	GTGCAGCTCT	CTCCTCTTTG	GGTCTTTGTC
52401	TTTCAGACTC	TAGCACCTTA	ATACCCCCCA	AGCCTTGTCT	TATCAACTCA
52451	GGGAGTTGGC	CACACTCATC	TTCGGTTTCC	ATCCCTGCAC	CTCTTCAGTT
52501	CCCCATCCCC	GCACCATGGC	TTGCAAACTC	TCTCAAGACA	GGAGGCTGGG
52551	GCAGTTGCAG	GGCTTGCTCT	ATTGGTTTTT	TGTTTCTTAG	GGATTACTGT
52601	CTTTCAATTG	TGGATGTCTA	ATGTATTAAA	AACCATTAT	CTATTATATG
52651	TTTGATTTGG	CTCTTTGGTT	GTTTCAGGTG	CGGAATTAAA	TCTGGTTTCT
52701	GATACTCTGT	CTTGGCTGAA	AGCATACGTT	TTCAGTGCCC	ACTGCTGGAG
52751	AGGGGTGGAG	GGCACTCAAG	AGTTCCATTT	GGACATTGAG	TTAGAGAAGT
52801	TGTGAGAGTT	TACATACCTG	CTCTGGAGCC	TTTACCCAC	TGTTCCCTCT
52851	GCATGGAAAA	TGCTCTCCCC	AGACTGGCAT	ATGCCAAGGT	CCAATATCAT
52901	TCCAGGGCTT	AAATTGATTG	CCAGATAAGC	TTTGCCTGTA	TTACTCTCAC
52951	TCCCTACTCA	TTTTCTGTCC	TGTTATCCTA	TTTTGTTCCT	TTGATAGCAC
53001	TTAACACATT	CTGAAATTAT	GTCATTGCTT	AACTCATTTA	TTACCTATCC
53051	TACTCCAGTA	AAATGTAATT	TTCGTGTCAG	CAGGGACCTT	TCTGGTCATG
53101	TCCACTGTGC	TAACCCATTT	TGAGGGTTTC	TGGCCCCTGG	GGAGTGCTCA
53151	GTGTGAATTT	GTGGAGTGAA	TATTAAGATG	AAGATAATGC	TAAGTAGGCA
53201	GTTGGATATG	TGAGTCTGGA	GCTCAGAGGA	GAGGAAAAAGT	GAAGCCTGAA
53251	GATACACATT	TAAAGTCTC	TGCTTAACAG	TGGCATTTAA	ATCCATAGGA
53301	ATGAATGAAA	CCCCTTGAT	TAGGGAATAG	AAGAGCAGAT	GGCCCAAGAT
53351	AGGATGCTAA	GAAACCTCCG	AATATGGAGT	TCACATCTCA	GTTGTGCCCT
53401	TGAAATTCTT	GTCATCCACT	TTTAGTTTTT	TTCTCTTCCT	ACTTGAAATT
53451	GCCTACCAAT	TTTCAGAGCC	CTCTCCTTCC	TTTATACCGT	CATGAGTTGC
53501	GCACTTTGCT	TATTTTCTG	ATTAAGATCA	TAAGCCTCTT	AAGGGAAAGA
53551	TCCTGATGTC	AAAATTACAT	TCTTGAATTG	AATTGGGTTG	GACTGGAGTG
53601	GACTGGAGTG	ATAAGTATTG	TCACATTATA	GAATTCCACC	CACTGAAGTG
53651	CAAGTGTTAA	ATGTATTAAT	ATTTCAAGTT	AATGGATACT	CTGCCCAAGT
53701	TTTTAGTTAA	TTATTATTAA	CTTTCATTA	TAAAAGCTTG	TTTTTGTTAT
53751	TAAATCAATC	ATCAGATTTA	ACGCAGAAAT	CAACTCATGT	AAACATACAG
53801	TGAGAGAATT	GTATTTTTCT	CTAAATTTTC	AGGACATTGA	AAAAGACTTG
53851	AAACAAATGA	GGCTTCAGAA	CACAAAGGAA	AGTAAAAATC	CAGAACAGAA
53901	ATATAAAGCT	AAGGTAAGAA	ATACTTTTGT	CTTTGGGTTT	CATATTAAAT
53951	AGCTGGCTGG	GGAGCCACCT	TGTGATCTCG	GTTGCCTGCA	TGATTTTCCC
54001	CCTAGTATT	TATAGAAATT	CTCTATTTTG	TGATATGAGA	CCAATGGTTT
54051	TAAGAATCTA	TAATGTCAAA	CAAAATTGAC	CTAGGGAGTT	GTAATTTTAA
54101	GGCTTTTACT	GAATTGCTAA	ACTTTTTTTT	TTTTTTTGCT	TTCTCCTAGA
54151	AGGGGGTAAA	ATTTGAAATT	AATTTAGACA	AATGTATTTT	TGATGAAAAC
54201	ATCCTCCAAG	AGGAAGAGGT	ATGCCATTAA	GTCTAAATTT	CCATTAGTAG
54251	GTATCAGAAA	ATGCATATAT	CTTAATAGCA	TGTTTCATGA	AATTATTTCA
54301	CAGGCTGTAG	GGATAATTTT	TTTCAACTTT	TATTTTAGAT	TCAGGTGGTA
54351	CATGTGCAGG	TTTGTTACCT	GGATATGTTG	TGTGATGTTG	AGGTTTGGGA
54401	TATGAATGAT	CCCGTCACCC	AGGTATTGAG	CATAATACCC	AGTAGTTAGT
54451	TTTTCAAGCC	TTGCTTCCCT	CCTTCTTAC	CCCCACTGTA	GTAGCTCCCA
54501	GTATCTATTG	TTGCTATCTT	TATGTCCATG	AGTACCCAAT	GTTTAGCTCC
54551	CACTTATAAG	TGAGAACATG	CAGAATTTGG	TTTTCTATCC	CTATGTAATT
54601	GGTTTTCTAT	CCCTATGTAA	TTTGCTTAGG	ATAGTAGCCT	CCAGCTGCAT
54651	CCATGTTGCA	TGGACATGAT	TTTATTCTTT	TTTATGGCTG	CATAGTATCC
54701	CATGGTGAT	ATGTACCACA	TTTTCTTTAT	CCAGACCACC	ACTGATGGGC
54751	ACCTAGGTTG	ATTCCATGAC	TTTGCTATTG	TGAATAGTGC	TGGGATGAAC
54801	ATGTGAGTAT	ATGTGTCTTT	TTGGTAGAAT	GGTTTGTTTT	CTTTTGGATA
54851	TATACCCAGT	AATGGGATTG	CTGGGTGAA	CAGTAGTTCT	AAGTTCTTTG
54901	AGAAATATCC	AAACTGCTTT	CTACAGTGGT	TGAACTAATT	TACATTACAT
54951	TTCCGCCAAC	ACTACATAAG	CATTCCCTTT	TCTCTGCAGC	CTCGCCAATA
55001	TTTGTTTTTT	GACTTTTTAG	TAATAGCCAT	TCTGACTCGT	GTGAGATGGT
55051	GTCTCATTGT	GGTTTTGATT	TGTAGTTCTC	TGATAATTAG	TGATGATGAG

FIGURE 3S

55101	TATTCCTTTA	TATATTTGTT	GGCTGCTTGT	ATGTCTTCTT	TTGAGAAGTG
55151	TCTCTTTCTA	TCCTTTGTCC	ACTTTAAAAAT	TTGGGTTGTT	TTTTCTTGTT
55201	CAGTTAAGTT	CCTTATAGAG	TCTGGATATT	AGACCTTTGT	TGGATGCATA
55251	GTTTGCAAAT	ATTTTCTTCT	ATTCTGTAGG	TTGTCTATTT	ACTCTGTTGA
55301	TAGTTTCTTT	TGCTGTGCAG	AAGCTCCTTA	GTTTAATTAG	GTTCCACTTG
55351	TCAATTTTGT	TTTTGTTGCA	ATTGCTTTTG	AGGACTTAAT	CACAAATTCT
55401	TTCCCAAGGC	CCATGTTTAT	AATGGTGTTT	CCTAGGTTTT	CTTTTAGGAT
55451	TCTTATAGTT	TAAGGTCTTA	CTTTTAAATT	GTTAAGTCAT	CTTTAGCTGA
55501	TTTTTGTATA	CAGTGAAAGG	TAGGGGTCCA	GTTTCATTCT	TCTGCATGTA
55551	GCTAACCAGC	TATCCCAGCA	CCACTTATTG	GATAGGAAGT	CCTTTCCCCA
55601	TTGCTTATTT	TTGTGCAAT	TGTCAAAGAT	TATATGGCTG	TAGATGAGTG
55651	GCTTTATTTT	TGGGTTCTCT	ATTCTGTTCC	TTGGTTTATG	TGTTTGTTTT
55701	TGAACCAAGT	CCATACAGTA	TTGATTACTG	TAGTCTTATG	GTATAGTTTG
55751	AAGTTGGGTA	ATGTGACGAC	TCTGGCGTTG	TTCTTTTTCG	TTAGAATTAC
55801	TTTGCTATT	TGGGCTCTTT	TTTGTTTACA	TATGAATTTT	AGAATAGTTT
55851	TTTTTTTCTC	CAATCCTGTG	AAAAGTTACA	TTGGTAGTTT	GACAGGAATA
55901	GTGTTGAATC	TATAGATTAC	TTTGGGCAGT	ATGGCCATTT	TAATGATATT
55951	GATTATTCCA	ATCCATGCAT	GTGGCATGTT	TTCCATTGTT	TTTATGTCAT
56001	GTATGATTTT	TTTCTGTGTT	GTGTAGCTCT	TCTTGTAGAG	ATCTTTTACC
56051	TCCTTGGTTA	GATGTACTCC	TAGGTATTTT	ATTTTATTTT	TTGGTGGCTA
56101	TTGTAAATGG	GATTACGTTT	TTGATTTGGC	TCTCTGCTTG	AATGTTATTG
56151	GTGTATAGGA	ATCCTATTGA	TTATTGTACT	TCGATATTGT	ATCCTGAAAC
56201	TTTGCTGAAG	TTGTTTCATCA	GTTCCAGGAA	CCTTTGGGTC	GAGTCTTTGG
56251	GTTTTCAACC	TATAGTATCA	TAAGCGTGAA	GAGATGGTTT	GACTTCTTCT
56301	TTTCTTATTT	GGATGCCTAG	AATTTTAGAA	AATATTTCTA	GAAAAATGTT
56351	TGGTGCTCAA	GGCCAGGGAA	CGGTGGCTCA	CAGCTGTAAT	CCCAGCACTT
56401	TGGGAGGCTG	AGACGGGCAG	ATCATGAGAT	CAGGAGATTG	AGACCATCCT
56451	GGCTAACATG	GTGAAACCCC	ATCTCTACTA	AAAATACAAA	AAATTAGCTG
56501	GGTGTGGTGT	CACCCACCTG	TAGTCTCAGC	TACTTAGGAG	GCTGAGGCAG
56551	GAGAATCACT	TGAACCCAGG	AGGCAGAGGT	TGCAGTGAGC	TGAGATCGCT
56601	GTAATGCACT	CGAGCCTGGG	CAACAGAGTG	AGACACTGTC	TCAAAAAAAAA
56651	AAAAAGGGAA	AGAAAAATGT	TTGGTGTTCA	AATGAGTCCT	CCAAATACTT
56701	TTTATTCTCC	CATTTTATTT	TATTGGTGTT	ATTTCTTTAG	ATAAATTATT
56751	ACATTTTAAT	TTACTTTTCT	TAAATAAAAA	GAGCTATTTT	ACTCATAATA
56801	TTAATTTTTA	TCATAGCCAA	ATTAATAATAG	AAGACCTGAT	ACATTGTCAA
56851	CAACTAATAT	ACTGACCTAA	AAAATTGAAC	AGGTACCCTG	AAACCAGGCA
56901	CATTTATTTT	AGGTCTTAAT	TAGTTATTGA	TAACCTTAAG	TAAATCTCAT
56951	TTATGCATTT	GGGCTCTCCT	TGCCACAGCA	AGGAGTAAAT	ACAGTAAATC
57001	CAATACAGTA	AATCCAAATT	TCATTTTATT	AGTTGATTTT	AAAAATCTTT
57051	TTTATCCTGG	TTTTATCAGA	CCTATAACAA	ATGTCAAAAAT	TAATTGGTTT
57101	ATTTTTCAT	TTTACCTTTT	CTGAATTCAC	CTTTTAAGTC	AATATAAGTA
57151	TGAATAATTA	TACCTGATGC	TCAGTTTTTA	TTTAATGTTT	TTTATTAGCT
57201	TAAAACATTT	TCATGTTAGC	ATTTCTTATT	TTTATGAGCA	TTTGCTACAT
57251	AAAGACTTCA	TTAGAGTGGT	GATAGTTAGC	ATTACCTCTT	GTTCAACCAT
57301	AAATTCCTAA	ATGCCCCAGA	GGTGAGACAT	CAGAGTGGAG	CAGATCTGGG
57351	GACCTGCTTC	TGAGTGGGAA	CTTGAGAAGT	GGTACTCTCA	CAGAGCTTCT
57401	GTGAAGTGAG	GTGCTGACGT	TGCCCTGCTG	AAATGAAAGA	ATGGAGTCCA
57451	AAAAGTTTTA	ACTGCCACTC	TTTCTTATTC	TTTGCTTTGA	TCTGCGTGAA
57501	ACAGAAGTGT	TCATTTTGGT	ATTGACTACA	AAATACTAGG	AGCAGATTTA
57551	GGGAGCTGGT	TAAGAATGTT	GTACACTTAA	AACAGGGCAT	GAATGAGAAA
57601	AGCTTGAGAG	CACGTGAGAA	TGGAGCTGAA	GTGGAATACT	ATTGAAGTCA
57651	GAAAGTCTAG	ATAAAATTAA	GTTGCCTTAT	GACCAAGTCT	TGACACTGTT
57701	AACATGGAGA	AGAAATGAAA	ACATTTCTGT	TTTTATCTAA	CATAGCTCTA
57751	GTTTTAAAAAC	TCTATGGATT	TATTTGTTTT	GTAAACATTT	GTTGAATATT
57801	TACTATATAC	CTTGCTAATT	AATTTTACTA	GGAACACGAA	AATATGGTTT
57851	TTCTTTCTTT	CAAAATATGG	CTAATTTATC	ATGAAACACT	GTGGAATTGA
57901	TTTAGGCAAT	GGATATACCA	AATGAAACTT	TGACCTTTGA	GGATGGCATG
57951	AAGTTTAAGG	AATATGAATG	TGTAAAGGAG	CATGGAGATT	ATACAGACAA

FIGURE 3T

58001	AGCATTTGAA	AAACTTCACT	CCCCAGAAGC	AGGTATGTGT	TTCTTGAAAG
58051	TTGTAAATGA	GAAGGAACTG	TTTTATTAGC	AACCCATTTT	GAACCTCTGTC
58101	CCCATGCATC	TGCCTCGGCT	CCACTGTTAC	TTGACCCCTT	TCTGCCCTCT
58151	CTAAGCAAGG	CAGAAACACA	CTTATTATTG	TCCTGCCACC	CATGCAGTGG
58201	CCCACTCCC	TGAGATCCAG	CCCTCCTCTC	CTGCTCCATA	CCCACTCCCT
58251	CTTGCACTT	TGGCTTCTCC	CAGGAGCTCC	AGACTTACCA	GTCTTTCTCA
58301	TTGTCTTCTG	GGAAGCTCCA	TGGACAAGTG	TTGCCAGTAT	CTGAAACTCA
58351	GCTGTGTAAA	GTCAAGCTCT	TCTGTGCTCT	TCCCAGTGAC	CCTTTATTTT
58401	GGTTAGTGTC	ACAGATGCAA	CTGGCTGGGG	CCAGTGTTGT	GGGCAGTAAA
58451	AGAATTTATC	AACACAATTG	TAAGTAAAGA	AAGGCAGATT	TATTAAAGTA
58501	CAGAGATACG	TTGCAAGAGT	GCAATGGGCA	GCACAGCAGA	GAAGAGGCTG
58551	TCTGCTAAGA	GGCAGGGGCT	AGAGGGAAAGT	TTTATAGGGT	CATATTGGAG
58601	GAGCTACATG	CTGATAAGGT	GTGCAGATAA	GGTTTTGCTG	CTTGGGCTAC
58651	ATGTGGAAGG	AATGAGGTAT	TTGGGAACAG	GATGTGACAG	CAGCTTGTCT
58701	GTGATGAGTC	ATCTCTCAGA	ACAGTTGTTT	CCCCATCCCC	ACCCCCAACC
58751	TGGGACCCCT	CCCTTTTTGT	TGTTTTACTTA	TCTTATGAGA	ACTTCACAGT
58801	CAGTGCTGTC	ACCAGGGTGC	ACCCTTAGCA	TAGTGTCTAT	TCTGAGATGT
58851	CTCTGGATCT	TTCTCTTCTC	TTCACTTCTCT	CTGTTACTGG	TTTAGGGCTC
58901	TGTCATCTCT	CAGTAGTGTG	GTGTAGGCTT	CAGAGACAGA	TGGGAATTGA
58951	ATCTCAGCTG	TTGCTGCCAC	CTTCTGGTTA	TGTGACCTTT	CTTTCACAAG
59001	TTATTCCAAC	ACTGAATCTC	AGTTTTACCT	TAGGAACAGG	GGATAATAGT
59051	AGTAGGAATA	ACCACACAGG	GTAATTGTGA	GGACCAAAGT	GAGTTTTGAT
59101	GTATAAACGA	CCTGGCACAT	ACTAGGTGCC	TAAATTAAGT	GCTGTCTTTT
59151	CATTTTCCCT	TTTCTTCCCC	CTTGCTGTAT	TGCCTTATTT	GCTTATGTGA
59201	CCTTCTTTCT	CTAGTATTTT	CCCTTCATTC	TCTAAATGGT	TACTGTATTA
59251	GTCCATTTTC	TTGCTGCTGA	TAAAGACATA	CCTGAGACTG	AGCAATTTAC
59301	AAAAGAAAGA	GGTTTAATTG	GACTTACAGT	TCCACATGGC	TGGGGAAGCC
59351	TCACAATCAT	GGTGGAAAGC	AAGGAAAAGC	AAGTCACATT	TTACATGGAT
59401	GGCAGCAGGC	AAAGAGAAAG	AACTTGTGCA	GAGGAACTCC	TCTTTTTAAA
59451	ACCATCTTAT	CTCGTGAGAC	TCATTACCA	TCACGAGAAC	AGCATGGGAA
59501	AGATCCGCCC	CCATGATTCA	ACCACCTCCC	TCTGGGTCAC	CCCACAACAC
59551	ACAGGAATTC	AAGATGAGAT	TTGGGTGGGA	CACAGCCAAA	CGATATCAGT
59601	TACTAAAGTT	ATCTTGGCAT	ATTATTACTC	TGCTCAGATT	TTTTTTTTTG
59651	ATAATACCTG	CAGAATAAGG	TCCATTCCAC	ATATTATCAC	ATTTAACT
59701	ACATGGCCTA	ATTCTGCTGT	GACCCACTTT	TCTCATCCCA	GCATGGCCTC
59751	TTTCTTTCCA	TGGAATGG	GATCCATACA	GCCTGCTGGA	ATGCCCATTT
59801	TCTCCTACAG	CTGGAATGCC	CATTTTCTCC	TACAGCATTT	ACAGAAGTGA
59851	CTTGGCTCAG	TTTCTCTTTC	CTGGAATACT	CTCTGCCTCA	TTTCTTCTG
59901	GAAAAATCTC	CATTACAGCAG	GCATCTTATT	GAGGATCTCC	TTTGTGCCAA
59951	AGACTGCTCA	CTGGTAGGGA	GCTCAAAGAT	GAATGAAATC	TGGGCCCTGT
60001	TCTCAATATC	ACAGAAGTGT	TATGAGCAAA	AAAGTCACAA	AACATGTTTT
60051	CTGAGCCTGA	AATGTTAATC	ACTGTTTGAA	GTGCGAGCTG	GGTGGAGAGT
60101	CAGGGAGGTC	CGCACTCCTC	CAGGGCTTCA	CATGCCATCA	TTTTTGTGAT
60151	TGAGAAGGAT	CATGCTGGCT	GCAGAGCAAA	GGATGGCATG	GAGGGCAAGA
60201	CTGAAGGCAG	GAGAAGAGTC	CAAGTGCATG	AGCCAGAGTG	GTGCAGGGAG
60251	AATAGATACT	GAGTGTGGGA	ACTGAGGAAG	AGAAGGGGCT	CAAGGATATT
60301	CCCAGTTTTT	TAATTCAAAT	GCATGAAGCT	TTCATCAACC	AAAAATACAT
60351	CACATGGAGG	GTAATGGGGT	CGGGAGAGAC	AAGGTAGTGA	TCTAAATTTG
60401	GAACATGTTG	AGATTTAGGT	CTATAGAGCA	TCAGTTGCAG	ATTCTATATA
60451	AGACTGAAGG	CCTGGGGCAT	ATCAGGGATA	AAGATATAGC	TTGGTGGCCC
60501	TTAGCATATC	CGTGGTTTTT	AACTTTGGTG	ATGGTCAAAA	TACCTATGCA
60551	GAAGGACTGG	AGTGAGAAGG	AAATGGAGCT	TAGGACATAA	CCCTACCACT
60601	ATATAAACAA	ACTTTGGAGA	ATCAGGAGAG	AGTAAAGCCA	AAGGAGGAGA
60651	GACAGGTCAT	GGAGGAGGCA	CAGGAATTGG	CAGCATCAAC	TGGAAGAGAA
60701	AGGCCAGATG	AGGTGAGTGG	GATTTGGCCC	TTCAGGAGCC	GTTAATGGCC
60751	TCAGGGAAAG	CAGTCAACTG	TGTAAGGGGT	AAATTCAATG	GTTATCTTTG
60801	CATCAGTTTG	CTGGGAAAAG	CAGAGGGGGT	TGGCTGTTTT	TTAGATGAAA
60851	GAAAAAATAA	CCTTCATCAG	TAGTATACTG	AAAATTGTCT	CTCATTTTAA

FIGURE 3U

60901	TCTGTATTCC	TGTAATTATT	ATTTAGGCTG	AAGGATTTTT	CCGTATGTTT
60951	GTTGACCATT	CATATTTCTC	CTTTTTTTTT	CTTTTTTCTT	TTTTTGTTTT
61001	TTTTTTGAGA	GGGAGTCTCC	CTCTGTCGCC	CAGGCTGGAG	TGCAGTGGCA
61051	CAATCTTGGC	TCACTGTAAC	CTCCGCCTCC	TGGGTTCAAG	CGATTCTCCT
61101	GCCTCAGCCT	CCCTGAGTAG	CTGGCATAGG	TGCGCGCCAC	CACGCCTAGC
61151	TGATTTTTAA	AATATTTTTA	GTAGAGATGA	GGTTTCACCA	TGTTTGCCAG
61201	GCTGGTATTT	GAACCTCTGA	TCTCAGGTGA	TCTGCCCACC	TTGGCCTCCC
61251	AAAGTGCTGG	GATTACAGGC	ATGAGCCACC	ACGCCTGGCC	AACCCTTCAT
61301	ATTTCTGTTA	TGAATTATGT	ACTCATGCCC	TTCATCCTTT	TTTCTACTGA
61351	AAATGGCATG	TTTGTTTTTT	TCTTTATAAG	ACTGATTTAA	ATCAAACCTT
61401	TGCCTGTAAT	ATGTATTGCA	AATGTTTTCC	TCAGTTGGTT	GTCAGATCTC
61451	ATTTATAGTA	ATAACAGCAA	ATATATATGA	GTGTGTGTGT	GTGTGTGTGT
61501	GTGTGTGTGT	GTGTATTTGT	GTATTCATCC	ACTTAGGAAT	AAATTTTATG
61551	AGAATTGTGC	GGCATATTAGA	AAGAAAACTG	TAAAACTTA	CTGAGGTATT
61601	TACAGACCAC	TTGAATAAAT	GGAGAGAAAT	AACGGTGCTA	TATATTGGAA
61651	ATATTTTTTC	CAAATAAATA	TTGCAGTATC	GTTGTCTGAG	GTATTACCCA
61701	GAACCTTTTG	TCTCACGACC	AAAAGAATAA	GGAGGGTGGA	CAGTAAGGGT
61751	GAGTTTGGAC	CGAAAAATTA	ATAAACAAAA	GAGGAAAGCT	CTTCACTGTG
61801	GAGAGGGGAC	CCAAGAGGGT	TGCCATTTCA	CAGCTGAGTA	CAAAGGCTTT
61851	TATGAGGAAC	CTGATAGGGC	TGGGGGTTTT	ATTTGCATAA	GGCATGAATT
61901	TCTGGCAGCT	CCACCCTGTT	CTCCTAGTAT	GCTGACTGGC	TAGGGGTTGT
61951	TTTTGGAAAA	GGCACCCTC	AGAAAATGAC	ATGATGGTTG	ACCAGGCATG
62001	GTAGTTTCATG	CCTGTAATCC	CAGCACTTTG	GGAGGCTGAG	GTGGGCAGAT
62051	CTCTCAAGGC	CAGGAGTTCG	AGACTAGCCT	GGCCAATATG	GCTAAAGCCC
62101	ATCTCTACTA	AAAATACAAA	AATTAGCCAG	GTGTGGTGGT	GCACACCTGT
62151	AATCTCAGCT	ACTTGGGAGG	CTGAGCCACA	AGAATCACTT	GGACCTGGGA
62201	GGTGAAGGTT	GCAGTGAGAC	GAGATTGTGC	CACCACACTC	CAGTCACACT
62251	CCAGCTGGGT	GACAGAGCAA	GCAAGACTCC	ATCTCAAAAA	AAAAAAAAAAAA
62301	AAAAATGACG	TGGTGTAAAG	ACCAGTTGGA	GCCTTGCCCC	ACAACCAGCT
62351	GAGTGTGGGA	GTGATGGTTC	ACAGAGGCTT	GGCTCACAGT	CCAAAGTATG
62401	CCCCAAAAAG	GAAAGGAATG	TGCTCACTGG	GGCCCACCAT	GTACATGCCC
62451	ACAAAAGGAG	AAGGAACTAT	TTGCTAGAGG	CCCCTGATT	GCACAAAGAA
62501	CAAAGGCATT	TCTGTGTTGG	ACTTTGCTCC	CTTATCTGTG	CAGCTGTGGG
62551	CATGTTTTAG	GCAAGCTTCC	TGTGCTAGTT	CCCTTATCTG	TGTCTGCAGC
62601	TTGATTTTTC	AGACTGTTCT	TTTGTTTGAA	AGAATTCTGA	GGACCTGCCC
62651	TAATGCCTG	CCTAATGAT	TCTTTCTTTC	TCCTCCCTCA	ATATGTGGAT
62701	TTATGGCTAT	TTCAATCAAA	ACCACAGTAG	GATTTTTTTT	TTAATGGTAT
62751	AGGGAGATCT	TGGCAGGTTG	GAGAATCCTG	GAGCTTCTTA	AGTGGCCAAA
62801	AATTTTGAAA	AAGAAGAACA	GTGAAGTGGT	ACTTACATTT	CCAAATGTCA
62851	AAATATATTA	CAGAAATTAT	AGTCATTAC	ACAATATGAT	AGTAGCACCC
62901	AAATAGTTAA	AACAGTGAGA	AGAGAAAGTT	AGAAACAGAT	CCTAGTATGT
62951	ATCATAATTC	AGCACAAATG	AAAAGTAACA	TCACAAGTCA	GCCTGAAAAG
63001	AAAGGATTAT	TCAGATAAAT	GCTGCTGGGC	CAATTGGTTA	ACAGTTTGGG
63051	GAAGATTGTG	AAATCAGACC	CTATATAATA	TGATACAACA	AAATAAATTT
63101	TTTAAAAAAG	AGTTATATGT	AAAAAGTTAT	ACATTAGAAA	ATGAAATAAA
63151	AGAACATAGG	TCATTTTTTT	TTTTTTTTGA	GACAGCGTCT	CACTCTGTCA
63201	CCAAGGCTGG	AGTGCAAAGG	CGTGATCTCG	GCTCACTGCA	AACTCCGCCT
63251	TCTGGGTTCA	AGCGATTCTC	CTGCCTCAGC	CTCCCGAGTA	GCTGGGACTA
63301	CAGGCACCCG	CTACCACGCC	CAGCTAATTT	TTATATTTTT	GATAGAGACG
63351	GGGTTTCACC	ATGTTGGCCA	GGATGGTTTC	GATCTCTTGA	CCTTGTGATC
63401	CGCCCGCCTC	GGCTCCCAA	AGTGCTGAGA	TTACAGGCGT	GAGCCACTGC
63451	ACCCGGCCGA	GTTAATTTTT	TTTGAACAGG	GAAGAGCTAT	CTGTTCAAAA
63501	TACATAGAAA	AAAAAACAC	AGAATAAATT	AGTAATAATT	CAACTTTAAC
63551	AACAAAAAGC	TGTAATAAAG	CAAATCATAC	TAACCCCT	(SEQ ID NO:3)

FIGURE 3V

FEATURES:

Start: 2012
Exon: 2012-2128
Intron: 2129-10078
Exon: 10079-10175
Intron: 10176-17356
Exon: 17357-17454
Intron: 17455-19144
Exon: 19145-19228
Intron: 19229-19311
Exon: 19312-19382
Intron: 19383-21317
Exon: 21318-21404
Intron: 21405-25173
Exon: 25174-25228
Intron: 25229-27433
Exon: 27434-27634
Intron: 27635-27711
Exon: 27712-27793
Intron: 27794-29849
Exon: 29850-29983
Intron: 29984-36496
Exon: 36497-36678
Intron: 36679-40418
Exon: 40419-40485
Intron: 40486-42286
Exon: 42287-42403
Intron: 42404-43377
Exon: 43378-43464
Intron: 43465-53832
Exon: 53833-53913
Intron: 53914-54149
Exon: 54150-54218
Intron: 54219-57905
Exon: 57906-58032
Intron: 58033-59835
Exon: 59836-59963
Intron: 59964-60551
Exon: 60552-60587
Stop: 60588

Chromosome map:
Chromosome 13

FIGURE 3W

Allelic Variants (SNPs):

DNA Position	Major	Minor	Domain	Protein Position	Major
<u>Minor</u>					
1848	A	G	Beyond ORF(5')		
1993	A	C	Beyond ORF(5')		
3796	C	T	Intron		
4854	C	G	Intron		
7649	A	G	Intron		
8491	G	A	Intron		
8928	T	C	Intron		
18844	A	T	Intron		
19055	G	A	Intron		
19607	G	C	Intron		
19935	G	A	Intron		
20595	T	G	Intron		
22513	C	G A	Intron		
25121	T	C	Intron		
25883	A	G	Intron		
26375	A	T	Intron		
26693	C	T	Intron		
30477	T	G	Intron		
30858	A	C	Intron		
31028	A	G	Intron		
37308	-	T G	Intron		
44213	G	A	Intron		
54046	G	A	Intron		
56598	A	G	Intron		
56759	A	T	Intron		
58510	A	G	Intron		
60356	G	A	Intron		
61643	C	T	Beyond ORF(3')		
62221	G	A	Beyond ORF(3')		
62306	A	- T	Beyond ORF(3')		
63224	G	T	Beyond ORF(3')		
63350	G	A	Beyond ORF(3')		
63517	C	A	Beyond ORF(3')		

Context:

DNA
Position

1848 TTTCCAGAAATCCCCCTAGGGGGCAGTACGTCCCCACTAAGAAAGGCTGAACTATAAAAAG
TGCACAAGCCTAAGGACATTCTGCTTTATAAAGGTGCGAAACACCGGATATAGTATCTT
TCATTCTCAGAACAACTTGCAAAACAGGTATTGTTATTCCATTTTAGAAATTAGGAAAG
TGAGGTTTGGCCAGTTAAGTGACTTACCCGAGAATACAGGGCAAAAGTGATCAAAGCT
GAGCTATGACCCGTGTCTGACCAAGAACTCTGTCTCATTTTCACTTATCTGTGGCCACAA
[A, G]
GAAAGTTATTTGTCTCTGTCTTGCAAGGCTGGGAGGAAAGTTTTAGCTAAGTGAGTTCT
TTTACACTTTAGTCATCAGTTTTCTGACTTTGTTAGTCTTTATGAGACGTGTGTGATAAA
TTTACATTACTCTAATTCAGGAAACTCAGCCATTGGAGACCATGGATAAGTACGATGT
GATTAAGGCCATCGGGCAAGGTGCCTTCGGGAAAGCATACTTAGCTAAAGGGAAATCAGA
TAGCAAGCACTGTGTCAAAAAGAGATCAATTTTGAAGGTAAGTTAAAGTTCAAATTT
1993 CAGGTATTGTTATTTCCATTTTAGAAATTAGGAAAGTGAGGTTTTGCCAGGTTAAGTGACT
TACCCGAGAATACAGGGCAAAAGTGATCAAAGCTGAGCTATGACCCGTGTCTGACCAAG
AAACTCTGTCTCATTTTCACTTATCTGTGGCCACAAAGAAAGTTATTTGTCTCTGTCTTGG
CAAGGCTGGGAGGAAAGTTTAGCTAAGTGAGTTCTTTTACACTTTAGTCATCAGTTTTT
TGACTTTGTTAGTCTTTATGAGACGTGTGTGATAAATTTACATTACTCTAATTCAGGAA
[A, C]

FIGURE 3X

CTCAGCCCATTTGGAGACCATGGATAAGTACGATGTGATTAAGGCCATCGGGCAAGGTGCC
TTCCGGGAAAGCATACTTAGCTAAAGGGAAATCAGATAGCAAGCACTGTGTCAATAAAGAG
ATCAATTTTGAAAAGGTAAGTTAAGTTCAAATTTCTGTTAATTTTCAGTGGGATATTCA
GCTGGCTTTTAAATCCAATATAAAAAGGAAATTTTTATTTTTATATTTTGAATTTTGAATTTTAA
CCATAATTGATTTTTGTAAATCAACCTCCTAAGTCCATTGTCCAAACAGCAACCAATGA

3796 TTACCACAAAAAATTTGCAAGAAACCTACCCAACTTAAAGCTCAAGAGTAGATGACTGG
CTTCCAGGGATAATGATTTATTTCCCAATATAGGTCTCTTTTTGTGAATCCATGGCATAT
TCATAATAATGTCCTCTTATTCTAGTGGCCCGCAATAGCTTCTCCCATGACATTATTCT
GCTCACTCTCTTTGTTTATCTGACTGCTCTCCCTCAGGCTTATCTCTGTCTTCGCCCTG
TGTATGTCCTCAACCATGTGTCCTTTCTGATTTTCTTTTTCTGTCCATTGTCACTAAA
[C, T]
TGCCCCACTTCAGTGTTTACCAATAAGTAGATCTCTCTTAAATCTCTGTCTCTACCCCTG
GCATCTTTTCAGTACCCTAGTTCTGCATTTCTTCTGCCAGCTAGATAAATTCAGGTAATAT
CTGTGGTTTTGTTTTGAGGTGGAGTCTCGCTCTGTGCCCCAGGCTGGAGTGCAGTGGTGC
CATCTCGGCTCACTGCAAGCTCTGCCTCCAGGTTTCATGCCATTCTCTGCCTCAGCCTC
CCGAGTGGTGTACAGGCGCCGCCACCAAGCTGGCTAATTTTTGTATTTTTAG

4854 CTTGAATTTGCTTCAGTCTTTTGTGCGAGGCCCTGGGTCACTTGGATCCTTCAAGTGGCT
CCAGCCCAATTTTGATAATGCTCCAGCCATGCCCCAAACCTTCACTGGGACAGAGGCTG
TAAAGAAAGAGTTGCTAGGTTTGTACTACATAAAAAATAGAAAACGTTTGTATGTCAAAAC
AAACACTATAAATAAATTCAAAGAAATCGAGAAGGTGCCAAAAATATTTGCAAGTATTGA
CTTAATGGTGTAGCCTTTTATTAATCAATAAAAAGATAAAATCCATATATGAAGTCAT
[C, G]
GTACAAAAATTTGAAACTCAGTAGAAAACTAAGAAATAGGAGTTTATTCAAAGAAAAAC
CCACAGATTAACACAGTTAGAAAAACAAATGTCCAACAGTAGGTAATTTGTTAAGTAATTTA
TAAAAAACTAAGTGGCTATTAGCAATCATGTTGTAGGTGAAGCATTGACATGGGAAAAAT
TCAATGTTTGAATGTTTGAAGAAATAGTAAGTGTAAATATAATCTTTGGAAAAAT
ATATATATTCTCCATATATATGTATACCTACAAATATGTTTATATATGTACAAAGAAAGA

7649 CATGATACTACATTGCCTCCCTTTATTTTTAATGACTGCATAGCATTAAAGTGGTAGCAG
GTCAAAAAATACCATAATTTAGCTGGGCATGGTGGCAAGTGCCTGTAGTCCAGCTATTCT
GGAGGATGAGTTGGGAGGATCCCTTGACCCAGGAGTTAAATCCAGCTTAGACAAACATA
GCAGAACTCTGTCTTAAAAAAGCTAGCAAAACACCCCTGTAAATTTATTTAA
CTCTTTTCTATTTTTCAGATAATTACATTGTTTGGTGGTTTTTGGCTACGATTCAATA
[A, G]
CATTTAATATGTAAGTATGATTCATTTTTATTAACAAAACTATGTATATATGCTTGCC
TATATATGCATGAAATAAAAAGCTCTAACTATTAACACAGTTATCCCTAGGGAATATAG
TATTAGGTGGCGCAAAAGTAATTGCATTTTGGCATTAAAGAGTAAGGTTACCACCTATG
GGCTTTGCTCTGTGGGCTAGATGAGAAAGAAAGAGGGAAGTTTCACTTTTACCTTATTCA
CTTCTATTTGACTTAAAAACAAGCGTGCAATTATTAGAGTAACCTAAAACTAGCAATAAAA

8491 GCCTGTGGTCTCAGCTACTCAGGAGGCTGAGGTGGGAGGATCACTTGAGCTCAGTGGGCA
GAGGCTCAGTGACCAAGATCATGCCACTGCACCTCAGCCTGGGTGATAGAGCAAGACC
TTGTCTTAAAAAAGATTTTCTTTCAGCAGGATACAGACCCCCACAAAAAT
GAACATTTTAAAGATTATATTATATTTGTAAGAACTGCCTTCCAGAAATATTTTATCA
ATTTGTGTAGTTTTACAGAAATAAATGAGTGTCCATTTTGTCTTCTGCGCAATAGT
[G, A]
GTTATTGACATTTCTTTTTCATCTTTGCCAGTTTCATACATGGAATACTATATTACATTTTG
TTTTAGCTTTTATTCCTTTTTTTTTTTTTTGTCAATGGAGTCTTACTCTGTCAACCCAGGC
TGGAGTGCAGTGGTGTGATTTTGGCTTACTGCAGCCTCCATCTCCAGGTTCAAGGGATT
CTCCTGCCTCAGCCTCCTGAGTAGTGTGAGACCACAGGTGTGTGCCACCACGCTGGCTAA
TTTTTTGTGTTTTAGTAGAGACAGGTTTTGTCTATGTTGGCCAGGCTGGTCTTGAACTC

8928 GATTTTGGCTTACTGCAGCCTCCATCTCCCAGGTTCAAGGGATTCTCCTGCCTCAGCCTC
CTGAGTAGCTGAGACCACAGGTGTGTGCCACCACGCTGGCTAATTTTTGTGTTTTTATG
TAGAGACAGGTTTTGCTATGTTGGCCAGGCTGGTCTTGAACCTCCTGGCCTCAAGTGATC
TGCCTGCCTTGGCTTCCCAAAGAGCTGGGATTACAGGCATGAGCTACCACACCCAGCCAA
ATTTTGTCTTAGTTTTATTCTTTGATTACTGCATGAGATTGAATTTTTTCTATCAG
[T, C]
CATTTTTATTTCTTTTTTTTTTTCGAGTTGACTATTCTTGTACTTTGCTATTTTTCTGTT
GGGTGTTTTGCCTTTTTAAAAATTTTATTTGCCATCAATTTTTATATTATAAATATATTTGT
CATATATGGTACAAATATTGTATCTTATCTTTTGTGTCTTTAATTTTGTATTATAAT
ATTCTTTTAAATAAATAGTAGTTAGGAATTTTTAAGTTGCTAAATGTATCCAGCTGGTA
GGAGTAATTTAGCTGTTTTTGTGTTTTGAAACTCCTATGTAAGTACTGACTATACAATTTAAATTG

18844 GAACACATTTTCATAAAGAGGCTCATGGTCAACAAAGATAAAATCAAAATCATGACTTAGA
AATAAACTAAACTTCAAGGTAAGTATTTGTTGGTTTTATATTAGATATACTGATATT
TTATTACAATTCCTAACCTCACAGATCCCCATTTCTTCTCTTCTCTCCCCACCCCTTG
TCACCCTCCTTCCACTGTAAAGGAAGAACCAATGGCTCCAGGTTATCAGGAACAGGGC

FIGURE 3Y

TGTAGCAAAGTTTGTGTGCTTTCTTTGACTAGAAATCTGACAAACTACAAATGGTTTTTC
 ATTTTACCTCTTATCTTCTAATAAGAATTGATGATATATCTGAAAGCATTTGTAAAAGCT
 GATCAACTTACATAAAATTGTAAGCGACACAAATTTAAGGCAGTGAAGGATAAAAGCT
 [T,C]
 TTATTAAGAATTATGGATATTTCTTGGCATGTAACTCTTATCTTCTTTAGGGATATTT
 GGTCTCTTGGCTGTGTCTTATATGAGCTCTGCACACTTAAACATCTGTAAAGTATGCTCA
 TTGTGAGACTAATCTTGAATTATTGGAATTGTAGAAAAGAAATTAACCTTCTGGGAGAAAA
 AGGTTAATGTTTGGTTTTATTAGATTGTTAAAAATTATATGGATAAGCTACTTAAAAATAA
 TGATAGATGACATGGAAAGCTGTCCAAGCAATATTATAAGTAAAAAGTCCAAGTTGGAG
 25883 TACTAAAAATACAAAAATTAGCCAGGCATGGTGGCATGTGCCTGCAGTCCCAGCTAGTTG
 GGAGGCTGAGGCACGAGAATTGCTAGAACCAGGAGGCAGAGGCTGCAGTCACTGAGAT
 TGGCCACTGCATCCAGCTGGGTGACAGCGAGACTCCATCTAAAAAAAATAATTAATT
 AATTAATTACTGTATGAATAGATACGTTTACGCAAAAAGAAAAATGTACATGGGCAAGTTC
 ATAGGAAACCAGGCACAAGCTTTAAGAGTCTTTCCAGAGGTACATGGGATGTGCCA
 [A,G]
 ATCTCCAGCATTTGTATCCACGTCACCTGTGAAATGTGATCTATAAGAAAGCTCATCGG
 ATATACCCAGTGGCCAGGATTTTTACTGGGGACTGGTCACATAGGCCACCTCTACCTGGC
 ATATGCCAACTTCCAGACTCTCGGAAAGAAAGCCCGTGTTCAGCATAAACCATTTTGT
 CACATAAATAGCTGAGGCAAGATAGCCACTTTGACATTACGGGAATGGTGGGAATTC
 TCTGAAATCTTAGTTCAGACACCAGCCACGGGCCAACATTGTAAGCAGGCTTTCTGA
 26375 CTGAGGCAAGATAGCCACTCTTGACATTACGGGAATGGTGGGAATCTTCTGAAATCTT
 AGTTCCAGACACCAGCCACGGGCCAACATTGTAAGCAGGCCCTTTCTGAGGAGAGCTTGC
 TACATCAACTCTTTCTCCACAGCTGTATCATTTGTTATTAATTATTGTCAAGGGTTGCA
 CAGCCAGTGTCTGACCAAAATGTGTACTCCATTGTTTTTTGAGATGGAGTCCCGCTCTG
 TTGCCAGACTGGAGTGGCGTGGCAGATCTCAGCTCACTGCAACCTCTGACTCCTGGGT
 [A,T]
 CAAGCAATTTCTTGGCTCAGCCTCCCGAGGAGCTGGGATTACAGGCACCCACCACCACA
 CCCGGCTAATTTTTTTGATTTTTAGTAGAGTCAGGGTTTTGCCATGTTGGCCAGGTTGG
 TCTTGAACCTCTGACCTTGGGTGATCTGCCACCTTGGCCTCCAGAGTGTGGGATTAC
 AGGCGTGAGCCACCATGCCCGGCCAATGTGTACCTTTATTGCTACACCATGGAGTTGAAT
 ATTATTATGTATAAATAACTATTGGTTTCAACAATAGAAGATTTCTGGTCTATGAAGCA
 26693 TCAGCTCCCGAGGAGCTGGGATTACAGGCACCCACCACCACCCGGCTAATTTTTTTG
 TATTTTTAGTAGAGTCAGGGTTTTGCCATGTTGGCCAGGTTGGTCTTGAACCTCTGACCT
 TGGGTGATCTGCCACCTTGGCCTCCAGAGTGTGGGATTACAGGCGTGAGCCACCATG
 CCCGGCCAATGTGTACCTTTATTGCTACACCATGGAGTTGAATATTATTATGTATAAATA
 ACTATTGGTTTTATACAATAAGAGATTTCTGGTCTATGAAGCATTTTAGAGGAAATTA
 [C,T]
 GATGTTTTATGTTAATTTTAAAAAGCAAGAGATAAAATTTTATATCAATATGACCTCAACT
 TTGTAAAAATAACATCATTTTTTAAAGAGATCAGAAGGAGCTATACCTCTGAGTGGTAAA
 ATTATACATATTTTCCCCTGTCTTTATAACTTCTTATACCTTCCAGTTTTTTTATTATGA
 GTAAACATATTTTGTATAAAGACAGAATTAACCAAAATAAAAACCTGTTTTAAATAA
 CATGGCATCTTGTGAATAACTGCAGTATCTGCTCATGAAAGATTAGTTGATGAAAACAA
 30477 TACAGACGTGTGCCACTATGCCAGCTAATTTTTGTATTTTTGGTAGAGATGGGGTTTCA
 CCATATTGGCCAGAATGGTCTCCATCTCTTGACCTCGTGATCCACCTGCCTGGGCTCCC
 AAAGTGCTGGGATTACAGGTGTGAGCCATGGCGCCCGGCCCGGCTAATTTTTTACTTT
 TAGTAGAGACAGGGTTTACCATGTTGGTCAAGCTGGTCTCGAACTCTGACCTTGGCAT
 CAGCCTGGCTCGGCTCCCAAGTGCTGGTATTACAAGCATAAGCCACTGCACCCAGCTG
 [T,G]
 TATATTCTTTTTCTTTAATTTTTTAATTAATAAAAAAATTTTTGTGGGTACATAGTAAGT
 GTATATATTTATGGGGTATATGAGATGTTTTGATACAGGCAAGCAATGTGAAATAAGCAC
 ATCATGGAGAATAGGGTGTGTGCTCCCTCAAGTATTTATCCTTTGAGTTACAAACAACCC
 AGTTATACCTGTGAACCTATTTCAAAATGTACAATTAAGTTACTATTGACCATAGGCAGT
 CTATTGATCTATCAAAATAGTGGTCTTATTCTTTGTTTTTTTAAACCATTAAGCT
 30858 TGAGATGTTTTGATACAGGCAAGCAATGTGAAATAAGCACATCATGGAGAATAGGGTGT
 TGTCCCTCAAGTATTTATCCTTTGAGTTACAAACAACCCAGTTATACTCTGTAACCTTAT
 TTCAAATGTACAATTAAGTTACTATTGACCATAGGCAGTCTATTGTGCTATCAAATAGT
 AGGTCTTATTCATTCTTTTGTTTTTTAACCCATTAAGCTATGGTATATTCTGACAGACC
 TATCTGCACATGTTATGAGGTACAAGCTTATTGTTTGGAGTCCACAAATTTGTACTTA
 [A,C]
 AATGAAGTATTCTGTACTGAGCATTATAATGGTATTTTGTGGACAACCTCTAGTTTTTA
 TATTTTATGAAACAATGCTGTATGCTCTTATAAGTATACTTTAGGCTTAATTTCTTTTT
 ATAACGAAATCTTCTAATTTCTAATAAATAAGATTTTTCTGTATAGGAAAAGTGAGTA
 ACATAGCAACAGAAAACACTCTGCATTTAATATTCTTAATTCTAACATATTATGTATAGG
 ATTGAGAAGTTTTATGATATAATAATTGATATTTCCCTAGTGATTCTTTGTGTTAATT
 31028 ATCAAATAGTAGGTCTTATTCATTCTTTTGTTTTTTTAACCATTAAAGCTATGGTATATT

FIGURE 3AA

CTGACAGACCTATCTGCACATGTTTCATGAGGTACAAGCTTATTGTTTGGAGTCCACAAAT
TTTGTACTTAAATGAAGTATTCTGTACTGAGCATTATAATGGTATTTTGTGGCAACT
TCTAGTTTTTATATTTTATGAAACAATGCTGTATGCTCTTATAAGTATACTTTAGGCTTA
ATTTTTCTTTTTATAACTGAAATTCCTTAATTTCTAATAAATAAGATTTTTCTGTATAGG
[A, G]
AAAGTGAGTAACATAGCAACAGAAAACACTCTGCATTTAATATTCTTAATTTCTAACATAT
TATGTATAGGATTGAGAAGTTTTTATGATATAATAATTGATATTTCCCTAGTGATTCTTT
GTGTTTAAATTTTGAATTCACCTCAGCAGAGTGTTGAATCTTTTAGGTACACTAGTGA
AATGCTTCTGGTATGTAATGATAAAATGGCTACTGTCTTTAATTAAGAAATTGTATTT
TTAAAGAAGGCTCATGGTTAAATTAAGAACCATTGGAAGTGATTTACTAAGTGTTTAC

37308 TAGTAAAGACAGGGTTTACCATGTTGGCCAACTGATCTTGAACCTCTGACCTCAGGTG
ATCTGCCCGCCTCAGCCTCCCAAAGTCTGGGATTACAGGCATGAGCCACCATGCTGGC
TCCATCTCCCAAGGCTCTAGAGTTGGCACAGATCACTGCTTCTCAGAAGAGCTTC
CATGTTAGTCCCTTCTTTCTATGTGAGCCCTATACCTGCTTGTAGTTGGTCTTCAAAT
TCTCAGGTACCCTCTCACCAGGCAGCCACTGACCTCATGTATCCACCTGCCCTGGCCTC
CTAAAGTCTGGGACTACAGGCAAGAGCCACTATTCCCAGCCTTTCTTTCTTTTTTTTT
[-, T, G]
TTAGAAAGATTTTGTTTTTATTTCCATCAGAATGTCATATATGTTACACAAATCAAATCT
GTTGACATCTCAAGCTTATAACAATTACGTGTTCTTATAAAATTACGTGGGAATTACATGT
ACTGTGAGAAGTGTTGTAATTATGATGTAATGTATATTATAATTTAGCCTACAGAAGTAA
CAAAGTCTTGTAATTAATAAGCAATAAATGTGTTGATAGATTATTACAATGTATAAGT
AATTGATAAATTATCTTTCTTTTCTGTAAACCCTTCTCATCTCAAGTCTGATAGCTT

44213 GAGTGCAGTTGAACTGATTCTTAAAAATCTCTTAAAGGCGCCACATTGGAAATTCATCCT
ACATGAAATAGCCAGCCTGTGTTTGGAAACCATGTTGTAAGAAAGACACATGGCTATTGA
AACACTAGGAACACACTCAGTGCCCTGGAATGCTCTCCTAGGAGAAGCTTGCAGGCACTG
AGACAGCTGTCTCCATCCACATGCACTTGGCCACACACTCATTGAGTAGAGCTACCAT
[G, A]
CTGCTGAAATGATCTCTCTCTCTTTCTCCACCGCAGTGTCATACAGATAAAATTCATA
TAAGTCAAATGAATGTATGGTGCAATTCAGTTGTGTTGGCAGGCATGAAC TAGAGCTT
TCACATACTGTATTAGTCTGCTCTCATACTGCTAATAAAGACATACCCAAGACTGGGTAA
TTTATAAAGAAAAAGAGGTGTAATAGACGCACAGTTTCACATGGCTGGGGAGGCCCTCACA
ATCATGGCAGAAGGCAAAGGAGGAGCAAAGTCATGCCTTACATGAAGGCAGGCAAGAGAG

54046 GTTATTAATCAATCATCAGATTTAACGCAGAAATCAACTCATGTAACATACAGTGAGA
GAATTTGATTTTTCTCTAAATTTT CAGGACATTGAAAAAGACTTGAAACAAATGAGGCTT
CAGAACACAAAGGAAAGTAAAAATCCAGAACAGAAATATAAAGCTAAGGTAAGAAATACT
TTTGTCTTTGGGTTCCCATATTAATAGCTGGCTGGGGAGGCCACCTTGTGATCTCGGTTGC
CTGCATGATTTTCCCCCTAGTATTTTATAGAATTGCTCTATTTTGTGATATGAGACCAAT
[G, A]
GTTTTAAGAATCTATAATGTCAAACAAAATTGACCTAGGGAGTTGTAATTTTAAGGCTTT
TACTGTAATTGCTAAACTTTTTTTTTTTTTTTTGGCTTCTCCTAGAAGGGGTAAAAATTTGA
AATTAATTTAGACAAATGTATTTCTGATGAAACATCCTCCAAGAGGAAGAGGTATGCCA
TTAAGTCTAAATTTCCATTAGTAGGTATCAGAAAATGCAATATATCTTAATAGCATGTTTC
ATGAAATTTATTTACAGGCTGAGGGATAATTTTTTTCAACTTTTTATTTTAGATTACAGT

56598 TCTTTTCTTATTTGGATGCCTAGAAATTTAGAAAATATTTCTAGAAAAATGTTTGGTGCT
CAAGGCCAGGGAACGGTGGCTCAGAGCTGTAATCCAGCACTTTGGGAGGCTGAGACGGG
CAGATCATGAGATCAGGAGATTGAGACCATCCTGGCTAACATGGTGAAACCCCATCTCTA
CTAAAAATACAAAAAATTAGCTGGGTGTGGTGTCACCCACCTGTAGTCTCAGCTACTTAG
GAGGCTGAGGCAGGAGAATCACTTGAACCCAGGAGGCAGAGGTTGCACTGAGCTGAGATC
[A, G]
CTGTACTGCACTCGAGCCTGGGCAACAGAGTGAGACACTGTCTCAAAAAAAAAAAAAAGGG
AAAGAAAAATGTTTGGTGTTCAAATGAGTCTCCAAATACTTTTTATTCTCCCATTTTAT
TTTATTGGTGTTATTTCTTTAGATAAATTATTACATTTTAAATTTACTTTTCTTTAAATAA
AAGAGCTATTTTACTCATAAATTAATTTTTATCATAGCCAAATTAATAAGAACCTG
ATACATTGTCAACAACTAATATACTGACCTAAAAAATTGAACAGGTACCCTGAAACCAGG

56759 TGGTGAAACCCCATCTCTACTAAAAATACAAAAAATTAGCTGGGTGTGGTGTCACCCACC
TGTAAGTCTCAGCTACTTAGGAGGCTGAGGCAGGAGAATCACTTGAACCCAGGAGGCAGAG
GTTGCAGTGAGCTGAGATCGCTGTACTGCACTCGAGCCTGGGCAACAGAGTGAGACACTG
TCTCAAAAAAAAAAAAAAGGGAAAGAAAAATGTTTGGTGTTCAAATGAGTCTCCAAATAC
TTTTTATTCTCCCATTTTATTTTATTGGTGTTATTTCTTTAGATAAATATTACATTTTA
[A, T]
TTTACTTTTCTTTAAATAAAAGAGCTATTTTACTCATAATATTAATTTTTATCATAGCCA
AATTAATAATAGAGACCTGATACATTGTCAACAACTAATATACTGACCTAAAAAATTGAA
CAGGTACCCTGAAACCAGGCACATTTATTTTAGGTCTTAATTAGTTATTGATAACTTTAA
GTAATCTCATTTATGCAATTTGGGCTCTCCTTGCCACAGCAAGGAGTAAATACAGTAAAT
CCAATACAGTAAATCCAAATTCATTTTATTAGTTGATTTCAAATCTTTTTTTATCCTG

FIGURE 3BB

58510 CTGAGATCCAGCCCTCTCTCTGCTCCATACCCACTCCCTCTTGACGCTTTGGCTTCTC
CCAGGAGCTCCAGACTTACCAGTCTTTCTATTGTCTTCTGGAAGCTCCATGGACAAGT
GTTGCCAGTATCTGAAACTCAGCTGTGTAAAGTCAAGCTCTTCTGTGCTCTTCCAGTGA
CCCTTTATTTTGGTTAGTGTACAGATGCAACTGGCTGGGGCCAGTGTGTGGGCAGTAA
AAGAAATTATCAACACAATTGTAAGTAAAGAAAGGCAGATTTATTAAGTACAGAGATAC
[A, G]
TTGCAAGAGTGAATGGGCAGCACAGCAGAGAAGAGGCTGTCTGCTAAGAGGCAGGGGCT
AGAGGGAAGTTTTATAGGGTCAATTGGAGGAGCTACATGCTGATAAGGTGTGCAGATAA
GGTTTTGCTGCTTGGGCTACATGTGGAAGGAATGAGGTATTTGGGAACAGGATGTGACAG
CAGCTTGTCTGTGATGAGTCATCTCAGAACAGTTGTTCCCCATCCCCACCCCAACC
TGGGACCCCTCCCTTTTGTGTTTACTTATCTTATGAGAACTTACAGTCAGTGCTGTC

60356 CCTGAAATGTTAATCACTGTTTGAAGTGCGAGCTGGGTGGAGAGTCAGGGAGGTCCGCAC
TCCTCCAGGGCTTACATGCCATCATTTTTGTGATTGAGAAGGATCATGCTGGCTGCAGA
GCAAGGATGGCATGGAGGGCAAGACTGAAGGCAGGAGAAGAGTCCAAGTCATGAGCCA
GAGTGGTGAGGAGAATAGATACTGAGTGTGGAACTGAGGAAGAGAAGGGGCTCAAGG
ATATCCAGCTTTTCTAATTCAAATGCATGAAGCTTTCATCAACCAAAAATACATCACAT
[G, A]
GAGGGTAATGGGGTCGGGAGAGACAAGGTAGTGATCTAAATTTGGAACATGTTGAGATTT
AGGCTCATAGAGCATCAGTTGCAGATTCTATATAAGACTGAAGGCTGGGGCATATCAGG
GATAAAGATATAGCTTGGTGGCCCTTAGCATATCCGTGGTTTTTAACTTTGGTGATGGTC
AAAAATACCTATGCAGAAGGACTGGAGTGAGAAGGAAATGGAGCTTAGGACATAACCTTAC
CACTATATAAACAACTTTGGAGAATCAGGAGAGAGTAAAGCCAAGGAGGAGAGACAGG

61643 TCTACTGAAATGGCATGTTTGTTTTTTCTTTATAAGACTGATTTAAATCAAACCTTTG
CCTGTAATATGTATGCAAAATGTTTCTCAGTTGGTTGTCAGATCTCATTTATAGTAAT
AACAGCAAATATATAGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTATTTGTGT
ATTCATCCACTTAGGAATAAATTTTATGAGAATTGTGCGGCATATAGAAAGAAAAGTGA
AAACCTTACTGAGGTATTTACAGACCACTTGAATAAATGGAGAGAAATAACGGTGCTATA
[C, T]
ATTGGAAATATTTTTCCAAATAAATATTGCAGTATCGTTGTCTGAGGTATTACCCAGAA
CTCTTTGTCTCACGACCAAAAGAATAAGGAGGGTGGACAGTAAGGGTGAGTTTGGACCGA
AAATTTAATAAACAAAAGAGGAAAGCTCTTCACTGTGGAGAGGGGACCCAGAGGGTTGC
CATTTACAGCTGAGTACAAAGGCTTTATGAGGAACCTGATAGGGCTGGGGGTTTCATT
TGCAATAGGCATGAATTTCTGGCAGCTCCACCCTGTTCTCCTAGTATGCTGACTGGCTAG

62221 CTCCTAGTATGCTGACTGGCTAGGGGTTGTTTTTGGAAAAGGCACCACTCAGAAAATGAC
ATGATGGTTGACCAGGCATGGTAGTTTCATGCCGTGAATCCAGCACTTTGGGAGGCTGAG
GTGGGCAGATCTCTCAAGGCCAGGAGTTCGAGACTAGCCTGGCCAAATATGGCTAAAGCCC
ATCTCTACTAAAAACAAAAATTAGCCAGGTGTGGTGGTGACACCTGTAATCTCAGCT
ACTTGGGAGGCTGAGCCACAAGAATCACTTGGACCTGGGAGGTGAAGGTTGCAGTGAGAC
[G, A]
AGATTGTGCCACCACACTCCAGTCACACTCCAGCTGGGTGACAGAGCAAGCAAGACTCCA
TCTCAAAAAAAAAAAAAAAAAAATGACGTGGTGTAAGACAGTTGGAGCCTTGGCCCA
CAACCAGCTGAGTGTGGAGTGATGGTTACAGAGGCTTGGCTCAGAGTCCAAAGTATGC
CCCAAAAAGGAAAGGAATGTGCTCACTGGGGCCCAACATGTACATGCCCAAAAAGGAGA
AGGAACTATTTGTAGAGGCCCACTGATTGCACAAAGAACAAAGGCATTTCTGTGTTGGA

62306 TCATGCCTGTAATCCAGCACTTTGGGAGGCTGAGGTGGGCAGATCTCTCAAGGCCAGGA
GTTTCGAGACTAGCTGGCCAATATGGCTAAAGCCCATCTCTACTAAAAATACAAAAATTA
GCCAGGTGTGGTGGTGACACCTGTAATCTCAGCTACTTGGGAGGCTGAGCCACAAGAAT
CACTTGGACCTGGGAGGTGAAGGTTGCAGTGAGACGAGATTGTGCCACCACACTCCAGTC
ACACTCCAGCTGGGTGACAGAGCAAGCAAGACTCCATCTCAAAAAAAAAAAAAAAAAAAAA
[A, -, T]
GACGTGGTGTAAGACCAAGTTGGAGCCTTGGCCCAACCAAGCTGAGTGTTGGAGTGATG
GTTACAGAGGCTTGGCTCACAGTCCAAAGTATGCCCAAAAAGGAAAGGAATGTGCTCA
CTGGGGCCCAACATGTACATGCCCAAAAAGGAGAAGGAATTTGCTAGAGGCCCACT
GATTGCACAAAGAACAAAGGCATTTCTGTGTTGGACTTTGCTCCCTTATCTGTGCAGCTG
TGGCATGTTTTAGGCAAGCTTCTGTGCTAGTTCCTTATCTGTGCTGCAGCTTGATT

63224 GAAAGTTAGAAACAGATCTAGTATGTATCATAATTCAGCACAAATGAAAAGTAACATCA
CAAGTCAGCGTGAAGAAAGGATTATTCAGATAAATGCTGCTGGGCCAATTGGTTAACA
GTTTGGGGAAGATTGTGAAATCAGACCCTATATAATATGATACAAACAAATAAATTTTTT
AAAAAGAGTTATATGTAAGGTTATACATTAGAAAAATGAAATAAAAGAACATAGGTCA
TTTTTTTTTTTTTGTAGACAGCGTCTCACTCTGTCCAAAGGCTGGAGTGCAAGGCGT
[G, T]
ATCTCGGCTCACTGCAAACTCCGCCTTCTGGGTTCAAGCGATTCTCTGCCTCAGCCTCC
CGAGTAGCTGGGACTACAGGCACCCGCTACCACGCCAGCTAATTTTATATTTTGATA
GAGACGGGTTTTACCATGTTGGCCAGGATGGTTTCGATCTCTTGACCTTGTGATCCGCC
CGCCTCGGCTCCCAAAGTGCTGAGATTACAGGCGTGAGCCACTGCACCCGGCCGAGTTA
ATTTTTTTTGAACAGGGAAGAGCTATCTGTTCAAAATACATAGAAAAAAACCACAGAA

FIGURE 3CC

63350 GGAAGATTGTGAAATCAGACCCTATATAATATGATACAACAAATAAATTTTTTAAAAA
 GAGTTATATGAAAAAGTTATACATTAGAAAAAGAAATAAAGAACATAGGTCATTTTTT
 TTTTTTTTGAGACAGCGTCTCACTCTGTCCACCAAGGCTGGAGTGCAAAGCGTGATCTC
 GGCTCACTGCAAACCTCCGCCTTCTGGGTTCAAGCGATTCTCCTGCCTCAGCCTCCCGAGT
 AGCTGGGACTACAGGCACCCGCTACCACGCCAGCTAATTTTTATTTTTTGATAGAGAC
 [G,A]
 GGGTTTCACCATGTTGGCCAGGATGGTTTCGATCTCTTGACCTTGATCCGCCCGCCTC
 GGCTCCCAAAGTGCTGAGATTACAGGCGTGAGCCACTGCACCCGGCCGAGTTAATTTTT
 TTTGAACAGGGAAGAGCTATCTGTTCAAAATACATAGAAAAAAACCACAGAATAAATT
 AGTAATAATTCACTTTAACAACAAAAAGCTGTAATAAAGCAAATCATACTAACCCT

63517 AAGGCGTGATCTCGGCTCACTGCAAACCTCCGCCTTCTGGGTTCAAGCGATTCTCCTGCCT
 CAGCCTCCCGAGTAGCTGGGACTACAGGCACCCGCTACCACGCCAGCTAATTTTTATAT
 TTTTGATAGAGACGGGTTTCACCATGTTGGCCAGGATGGTTTCGATCTCTTGACCTTG
 GATCCGCCCGCCTCGGCCTCCCAAAGTGCTGAGATTACAGGCGTGAGCCACTGCACCCGG
 CCGAGTTAATTTTTTTGAACAGGGAAGAGCTATCTGTTCAAAATACATAGAAAAAA
 [C,A]
 CACAGAATAAATTAGTAATAATTCACTTTAACAACAAAAAGCTGTAATAAAGCAAATCA
 TACTAACCCT

FIGURE 3DD